

122257 sequence listing May 10 2006.ST25.txt  
SEQUENCE LISTING

<110> Sutherland, Robert  
Henshall, Susan  
O'Brien, Philippa

<120> Methods of diagnosis and prognosis of ovarian cancer

<130> FBR0003-100

<140> US 10/526,979  
<141> 2005-03-07

<150> PCT/AU2003/001166  
<151> 2003-09-05

<150> AU 2002951346  
<151> 2002-09-05

<160> 84

<170> PatentIn version 3.3

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<212> DNA  
<213> homo sapiens

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<222> (94)..(2850)

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Met Glu Ala Pro Glu Tyr Leu  
1 5  
gat ttg gat gaa att gac ttt agt gat gac ata tct tat tca gtc aca 162  
Asp Leu Asp Glu Ile Asp Phe Ser Asp Asp Ile Ser Tyr Ser Val Thr  
10 15 20  
tca ctc aag acg atc cca gaa ctg tgc cga aga tgt gat acg caa aac 210  
Ser Leu Lys Thr Ile Pro Glu Leu Cys Arg Arg Cys Asp Thr Gln Asn  
25 30 35  
gaa gac aga tca gct tct agc tct agc tgg aat tgt ggc atc tca act 258  
Glu Asp Arg Ser Ala Ser Ser Ser Trp Asn Cys Gly Ile Ser Thr  
40 45 50 55  
ctt att aca aac acg caa aag ccc aca gga atc gct gat gtg tac agt 306  
Leu Ile Thr Asn Thr Gln Lys Pro Thr Gly Ile Ala Asp Val Tyr Ser  
60 65 70  
aag ttc cgc cca gtg aag cgg gtt tcg cca ctg aaa cat cag cca gag 354  
Lys Phe Arg Pro Val Lys Arg Val Ser Pro Leu Lys His Gln Pro Glu  
75 80 85  
act ctg gag aac aat gaa agt gat gac caa aag aac cag aaa gtg gtt 402  
Thr Leu Glu Asn Asn Glu Ser Asp Asp Gln Lys Asn Gln Lys Val Val  
90 95 100  
gag tac cag aaa ggg ggt gag tct gac ctg ggc ccc cag cct cag gag 450  
Glu Tyr Gln Lys Gly Gly Glu Ser Asp Leu Gly Pro Gln Pro Gln Glu  
105 110 115

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ctt ggc cct gga gat gga gtg ggc ggc cca cca ggt aag agc tct gag Leu Gly Pro Gly Asp Gly Val Gly Gly Pro Pro Gly Lys Ser Ser Glu 120 125 130 135	498
ccc agc aca tcg ctg ggt gaa ctg gag cac tac gac ctc gac atg gat Pro Ser Thr Ser Leu Gly Glu Leu Glu His Tyr Asp Leu Asp Met Asp 140 145 150	546
gag att ctg gat gtg cct tat att aaa tcc agt cag cag ctt gcc tct Glu Ile Leu Asp Val Pro Tyr Ile Lys Ser Ser Gln Gln Leu Ala Ser 155 160 165	594
ttt acc aag gtg act tca gaa aaa aga att ttg ggc tta tgc aca acc Phe Thr Lys Val Thr Ser Glu Lys Arg Ile Leu Gly Leu Cys Thr Thr 170 175 180	642
atc aat ggc ctt tct ggc aaa gcc tgc tct aca gga agt tct gag agc Ile Asn Gly Leu Ser Gly Lys Ala Cys Ser Thr Gly Ser Ser Glu Ser 185 190 195	690
tca tca tcc aac atg gca cca ttt tgt gtt ctt tct ccc gtg aaa agc Ser Ser Ser Asn Met Ala Pro Phe Cys Val Leu Ser Pro Val Lys Ser 200 205 210 215	738
cct cac ttg aga aaa gca tca gct gtc atc cac gac cag cac aag ctg Pro His Leu Arg Lys Ala Ser Ala Val Ile His Asp Gln His Lys Leu 220 225 230	786
tcc act gaa gaa acc gag atc tca cct cct ctg gtt aaa tgt ggc tct Ser Thr Glu Glu Thr Glu Ile Ser Pro Pro Leu Val Lys Cys Gly Ser 235 240 245	834
gca tat gag cct gaa aac cag agt aaa gac ttc cta aac aag aca ttt Ala Tyr Glu Pro Glu Asn Gln Ser Lys Asp Phe Leu Asn Lys Thr Phe 250 255 260	882
agt gat cct cat ggt cga aaa gtt gag aag aca aca cca gac tgc cag Ser Asp Pro His Gly Arg Lys Val Glu Lys Thr Thr Pro Asp Cys Gln 265 270 275	930
ctc agg gcc ttc cac cta caa tcc tca gca gca gaa tcc aaa cca gaa Leu Arg Ala Phe His Leu Gln Ser Ser Ala Ala Glu Ser Lys Pro Glu 280 285 290 295	978
gag cag gtc agt ggc cta aac cgg acc agc tcc caa ggc cca gaa gaa Glu Gln Val Ser Gly Leu Asn Arg Thr Ser Ser Gln Gly Pro Glu Glu 300 305 310	1026
agg agt gag tat ctg aaa aaa gtg aaa agc atc ttg aac att gtt aaa Arg Ser Glu Tyr Leu Lys Lys Val Lys Ser Ile Leu Asn Ile Val Lys 315 320 325	1074
gaa gga cag atc tct ctc ctg cca cac cta gct gca gac aat cta gac Glu Gly Gln Ile Ser Leu Leu Pro His Leu Ala Ala Asp Asn Leu Asp 330 335 340	1122
aaa att cac gac gaa aat gga aac aat cta tta cat att gcg gcg tca Lys Ile His Asp Glu Asn Gly Asn Asn Leu Leu His Ile Ala Ala Ser 345 350 355	1170
cag gga cac gca gag tgt cta cag cac ctc act tct ttg atg gga gaa Gln Gly His Ala Glu Cys Leu Gln His Leu Thr Ser Leu Met Gly Glu 360 365 370 375	1218
gac tgc ctc aat gag cgc aac act gag aag ttg act cca gca ggc ctg Asp Cys Leu Asn Glu Arg Asn Thr Glu Lys Leu Thr Pro Ala Gly Leu 380 385 390	1266

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gcc att aag aat ggt cag ttg gag tgc gta cgc tgg atg gtg agc gaa Ala Ile Lys Asn Gly Gln Leu Glu Cys Val Arg Trp Met Val Ser Glu 395 400 405	1314
aca gaa gcc att gca gaa ctg agt tgt tct aag gat ttt cca agc ctt Thr Glu Ala Ile Ala Glu Leu Ser Cys Ser Lys Asp Phe Pro Ser Leu 410 415 420	1362
att cat tac gca ggt tgc tat ggc cag gaa aag att ctt ctg tgg ctt Ile His Tyr Ala Gly Cys Tyr Gly Gln Glu Lys Ile Leu Leu Trp Leu 425 430 435	1410
ctt cag ttt atg caa gaa cag ggc atc tcg ttg gat gaa gta gac cag Leu Gln Phe Met Gln Glu Gln Gly Ile Ser Leu Asp Glu Val Asp Gln 440 445 450 455	1458
gat ggc aac agt gcc gtt cac gta gcc tca cag cat ggc tac ctt gga Asp Gly Asn Ser Ala Val His Val Ala Ser Gln His Gly Tyr Leu Gly 460 465 470	1506
tgc ata cag acc ttg gtt gaa tat gga gca aat gtc acc atg cag aac Cys Ile Gln Thr Leu Val Glu Tyr Gly Ala Asn Val Thr Met Gln Asn 475 480 485	1554
cac gct ggg gaa aag ccc tcc cag agc gcc gag cgg cag ggg cac acc His Ala Gly Glu Lys Pro Ser Gln Ser Ala Glu Arg Gln Gly His Thr 490 495 500	1602
ctg tgc tcc agg tac ctg gtg gtg gtg gag acc tgc atg tcg ctg gcc Leu Cys Ser Arg Tyr Leu Val Val Val Glu Thr Cys Met Ser Leu Ala 505 510 515	1650
tct caa gtg gtg aag tta acc aag cag cta aag gaa caa aca gta gaa Ser Gln Val Val Lys Leu Thr Lys Gln Leu Lys Glu Gln Thr Val Glu 520 525 530 535	1698
cgt gtc acg ctg cag aac caa ctc caa caa ttt cta gaa gcc cag aaa Arg Val Thr Leu Gln Asn Gln Leu Gln Gln Phe Leu Glu Ala Gln Lys 540 545 550	1746
tca gag ggc aag tca ctc cct tct tca ccc agt tca cca tcc tca cct Ser Glu Gly Lys Ser Leu Pro Ser Ser Pro Ser Pro Ser Pro 555 560 565	1794
gcc tcc aga aag tcc cag tgg aaa tct cca gat gca gat gat tct Ala Ser Arg Lys Ser Gln Trp Lys Ser Pro Asp Ala Asp Asp Ser 570 575 580	1842
gta gcc aaa agc aag cca gga gtc caa gag ggg att cag gtt ctt gga Val Ala Lys Ser Lys Pro Gly Val Gln Glu Gly Ile Gln Val Leu Gly 585 590 595	1890
agc ctg tca gcc tcc agc cgg gct aga ccc aaa gca aaa gat gaa gat Ser Leu Ser Ala Ser Ser Arg Ala Arg Pro Lys Ala Lys Asp Glu Asp 600 605 610 615	1938
tct gat aaa atc tta cgc cag tta ttg gga aag gaa atc tca gaa aat Ser Asp Lys Ile Leu Arg Gln Leu Leu Gly Lys Glu Ile Ser Glu Asn 620 625 630	1986
gtc tgc acc cag gaa aaa ctg tcc ttg gaa ttc cag gat gct cag gct Val Cys Thr Gln Glu Lys Leu Ser Leu Glu Phe Gln Asp Ala Gln Ala 635 640 645	2034
tcc tct aga aat tct aaa aag atc cca ctg gag aag agg gaa ctg aag Ser Ser Arg Asn Ser Lys Lys Ile Pro Leu Glu Lys Arg Glu Leu Lys 650 655 660	2082

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tta gcc agg ctg aga cag ctg atg cag agg tca ctg agt gag tct gac Leu Ala Arg Leu Arg Gln Leu Met Gln Arg Ser Leu Ser Glu Ser Asp 665 670 675	2130
aca gac tcc aac aac tct gag gac ccc aag act acc cca gtg agg aag Thr Asp Ser Asn Asn Ser Glu Asp Pro Lys Thr Pro Val Arg Lys 680 685 690 695	2178
gct gac cga cca agg ccg cag ccc att gta gaa agc gta gag agt atg Ala Asp Arg Pro Glu Pro Gln Pro Ile Val Glu Ser Val Glu Ser Met 700 705 710	2226
gac agc gca gaa agc ctg cac ctg atg att aag aaa cac acc ttg gca Asp Ser Ala Glu Ser Leu His Leu Met Ile Lys Lys His Thr Leu Ala 715 720 725	2274
tca ggg gga cgc agg ttt cct ttc agc atc aag gcc tcc aaa tcc ctg Ser Gly Gly Arg Arg Phe Pro Phe Ser Ile Lys Ala Ser Lys Ser Leu 730 735 740	2322
gat ggc cac agc cca tct ccc acc tca gag agc agc gaa cca gac tta Asp Gly His Ser Pro Ser Pro Thr Ser Glu Ser Ser Glu Pro Asp Leu 745 750 755	2370
gaa tcc cag tat cca ggc tca ggg agt att cct cca aac cag ccc tct Glu Ser Gln Tyr Pro Gly Ser Gly Ser Ile Pro Pro Asn Gln Pro Ser 760 765 770 775	2418
ggt gac cct cag cag ccc agc cct gac agt act gct gcc cag aaa gtt Gly Asp Pro Gln Gln Pro Ser Pro Asp Ser Thr Ala Ala Gln Lys Val 780 785 790	2466
gcc aca agt ccc aag agt gcc ctc aag tct cca tct tcc aag cgt agg Ala Thr Ser Pro Lys Ser Ala Leu Lys Ser Pro Ser Ser Lys Arg Arg 795 800 805	2514
aca tct cag aac tta aaa ctg aga gtt acc ttt gag gag cct gtg gtg Thr Ser Gln Asn Leu Lys Leu Arg Val Thr Phe Glu Glu Pro Val Val 810 815 820	2562
cag atg gag cag cct agc ctt gaa ctg aat gga gaa aaa gac aaa gat Gln Met Glu Gln Pro Ser Leu Glu Leu Asn Gly Glu Lys Asp Lys Asp 825 830 835	2610
aag ggc agg act ctc cag cgg acc tcc aca agt aac gaa tcg ggg gat Lys Gly Arg Thr Leu Gln Arg Thr Ser Thr Ser Asn Glu Ser Gly Asp 840 845 850 855	2658
caa ctg aaa agg cct ttt gga gcc ttt cga tct atc atg gag aca cta Gln Leu Lys Arg Pro Phe Gly Ala Phe Arg Ser Ile Met Glu Thr Leu 860 865 870	2706
agt ggc aac caa aac aat aat aat aac tac cag gca gcc aac cag ctg Ser Gly Asn Gln Asn Asn Asn Asn Asn Tyr Gln Ala Ala Asn Gln Leu 875 880 885	2754
aaa acc tct aca ttg ccc ttg acc tca ctt ggg agg aag aca gat gcc Lys Thr Ser Thr Leu Pro Leu Thr Ser Leu Gly Arg Lys Thr Asp Ala 890 895 900	2802
aag gga aac cct gcc agc tcc gct agc aaa gga aag aat aag gca gca Lys Gly Asn Pro Ala Ser Ser Ala Ser Lys Gly Lys Asn Lys Ala Ala 905 910 915	2850
taatgacatc aatagaaaaa tgaagaaatc ctacagcata aagcacattg ctgagccaga	2910
gtcaaaagaa ctcttcttgt aaatcacttt ttaaattttc tctcactgat gccctttgga	2970

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aattattgga aatttctgga ctatcctctt tggaagaga accatgaaaa caatgcctca	3030
ccagcagaag aacagaatat caggatgcct taaatttata gtagtagact gtaaaagatt	3090
cattttgggg tgatatctgt atatataact tgttttttta aaagatgccg tttaaaagca	3150
tgattgggaa aatgtacgtt ttttaagagt agattgattc accctaccca caggacattc	3210
accaagccac tgataccatt ttatatttca tcaattgcat gagtatttgc taatgttgat	3270
tgaacctccc tttccccata atgtgggcag atttggtcga gtccttcat gagatcaggt	3330
cagtgggtatt gtttctgtca agagtgtttt ttctgtcatt tctacttttt gtataaagga	3390
aataaaacaa tgттаacagc caaaaaaaaa aaaaaaaaaa aa	3432

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<400> 2

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Arg Arg Cys Asp Thr Gln Asn Glu Asp Arg Ser Ala Ser Ser Ser Ser	
35 40 45	
Trp Asn Cys Gly Ile Ser Thr Leu Ile Thr Asn Thr Gln Lys Pro Thr	
50 55 60	
Gly Ile Ala Asp Val Tyr Ser Lys Phe Arg Pro Val Lys Arg Val Ser	
65 70 75 80	
Pro Leu Lys His Gln Pro Glu Thr Leu Glu Asn Asn Glu Ser Asp Asp	
85 90 95	
Gln Lys Asn Gln Lys Val Val Glu Tyr Gln Lys Gly Gly Glu Ser Asp	
100 105 110	
Leu Gly Pro Gln Pro Gln Glu Leu Gly Pro Gly Asp Gly Val Gly Gly	
115 120 125	
Pro Pro Gly Lys Ser Ser Glu Pro Ser Thr Ser Leu Gly Glu Leu Glu	
130 135 140	
His Tyr Asp Leu Asp Met Asp Glu Ile Leu Asp Val Pro Tyr Ile Lys	
145 150 155 160	
Ser Ser Gln Gln Leu Ala Ser Phe Thr Lys Val Thr Ser Glu Lys Arg	
165 170 175	

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Ile Leu Gly Leu Cys Thr Thr Ile Asn Gly Leu Ser Gly Lys Ala Cys  
180 185 190

Ser Thr Gly Ser Ser Glu Ser Ser Ser Ser Asn Met Ala Pro Phe Cys  
195 200 205

Val Leu Ser Pro Val Lys Ser Pro His Leu Arg Lys Ala Ser Ala Val  
210 215 220

Ile His Asp Gln His Lys Leu Ser Thr Glu Glu Thr Glu Ile Ser Pro  
225 230 235 240

Pro Leu Val Lys Cys Gly Ser Ala Tyr Glu Pro Glu Asn Gln Ser Lys  
245 250 255

Asp Phe Leu Asn Lys Thr Phe Ser Asp Pro His Gly Arg Lys Val Glu  
260 265 270

Lys Thr Thr Pro Asp Cys Gln Leu Arg Ala Phe His Leu Gln Ser Ser  
275 280 285

Ala Ala Glu Ser Lys Pro Glu Glu Gln Val Ser Gly Leu Asn Arg Thr  
290 295 300

Ser Ser Gln Gly Pro Glu Glu Arg Ser Glu Tyr Leu Lys Lys Val Lys  
305 310 315 320

Ser Ile Leu Asn Ile Val Lys Glu Gly Gln Ile Ser Leu Leu Pro His  
325 330 335

Leu Ala Ala Asp Asn Leu Asp Lys Ile His Asp Glu Asn Gly Asn Asn  
340 345 350

Leu Leu His Ile Ala Ala Ser Gln Gly His Ala Glu Cys Leu Gln His  
355 360 365

Leu Thr Ser Leu Met Gly Glu Asp Cys Leu Asn Glu Arg Asn Thr Glu  
370 375 380

Lys Leu Thr Pro Ala Gly Leu Ala Ile Lys Asn Gly Gln Leu Glu Cys  
385 390 395 400

Val Arg Trp Met Val Ser Glu Thr Glu Ala Ile Ala Glu Leu Ser Cys  
405 410 415

Ser Lys Asp Phe Pro Ser Leu Ile His Tyr Ala Gly Cys Tyr Gly Gln  
420 425 430

Glu Lys Ile Leu Leu Trp Leu Leu Gln Phe Met Gln Glu Gln Gly Ile  
435 440 445

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Ser Leu Asp Glu Val Asp Gln Asp Gly Asn Ser Ala Val His Val Ala  
450 455 460

Ser Gln His Gly Tyr Leu Gly Cys Ile Gln Thr Leu Val Glu Tyr Gly  
465 470 475 480

Ala Asn Val Thr Met Gln Asn His Ala Gly Glu Lys Pro Ser Gln Ser  
485 490 495

Ala Glu Arg Gln Gly His Thr Leu Cys Ser Arg Tyr Leu Val Val Val  
500 505 510

Glu Thr Cys Met Ser Leu Ala Ser Gln Val Val Lys Leu Thr Lys Gln  
515 520 525

Leu Lys Glu Gln Thr Val Glu Arg Val Thr Leu Gln Asn Gln Leu Gln  
530 535 540

Gln Phe Leu Glu Ala Gln Lys Ser Glu Gly Lys Ser Leu Pro Ser Ser  
545 550 555 560

Pro Ser Ser Pro Ser Ser Pro Ala Ser Arg Lys Ser Gln Trp Lys Ser  
565 570 575

Pro Asp Ala Asp Asp Ser Val Ala Lys Ser Lys Pro Gly Val Gln  
580 585 590

Glu Gly Ile Gln Val Leu Gly Ser Leu Ser Ala Ser Ser Arg Ala Arg  
595 600 605

Pro Lys Ala Lys Asp Glu Asp Ser Asp Lys Ile Leu Arg Gln Leu Leu  
610 615 620

Gly Lys Glu Ile Ser Glu Asn Val Cys Thr Gln Glu Lys Leu Ser Leu  
625 630 635 640

Glu Phe Gln Asp Ala Gln Ala Ser Ser Arg Asn Ser Lys Lys Ile Pro  
645 650 655

Leu Glu Lys Arg Glu Leu Lys Leu Ala Arg Leu Arg Gln Leu Met Gln  
660 665 670

Arg Ser Leu Ser Glu Ser Asp Thr Asp Ser Asn Asn Ser Glu Asp Pro  
675 680 685

Lys Thr Thr Pro Val Arg Lys Ala Asp Arg Pro Arg Pro Gln Pro Ile  
690 695 700

Val Glu Ser Val Glu Ser Met Asp Ser Ala Glu Ser Leu His Leu Met  
705 710 715 720

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Ile Lys Lys His Thr Leu Ala Ser Gly Gly Arg Arg Phe Pro Phe Ser  
725 730 735

Ile Lys Ala Ser Lys Ser Leu Asp Gly His Ser Pro Ser Pro Thr Ser  
740 745 750

Glu Ser Ser Glu Pro Asp Leu Glu Ser Gln Tyr Pro Gly Ser Gly Ser  
755 760 765

Ile Pro Pro Asn Gln Pro Ser Gly Asp Pro Gln Gln Pro Ser Pro Asp  
770 775 780

Ser Thr Ala Ala Gln Lys Val Ala Thr Ser Pro Lys Ser Ala Leu Lys  
785 790 795 800

Ser Pro Ser Ser Lys Arg Arg Thr Ser Gln Asn Leu Lys Leu Arg Val  
805 810 815

Thr Phe Glu Glu Pro Val Val Gln Met Glu Gln Pro Ser Leu Glu Leu  
820 825 830

Asn Gly Glu Lys Asp Lys Asp Lys Gly Arg Thr Leu Gln Arg Thr Ser  
835 840 845

Thr Ser Asn Glu Ser Gly Asp Gln Leu Lys Arg Pro Phe Gly Ala Phe  
850 855 860

Arg Ser Ile Met Glu Thr Leu Ser Gly Asn Gln Asn Asn Asn Asn Asn  
865 870 875 880

Tyr Gln Ala Ala Asn Gln Leu Lys Thr Ser Thr Leu Pro Leu Thr Ser  
885 890 895

Leu Gly Arg Lys Thr Asp Ala Lys Gly Asn Pro Ala Ser Ser Ala Ser  
900 905 910

Lys Gly Lys Asn Lys Ala Ala  
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tgtggcagaa gggaccaagc agtggatatt gagcctgtga agtccaactc ttaagctccg 180



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agacctgggg gactgagagc ccagctctga aaagtgc	atg	aat	tcc	gga	gtt	235
	Met	Asn	Ser	Gly	Val	
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gcc atg aaa tat gga aac gac tcc tcg gcc gag ctg agt gag ctc cat						283
Ala Met Lys Tyr Gly Asn Asp Ser Ser Ala Glu Leu Ser Glu Leu His						
	10			15	20	
tca gca gcc ctg gca tca cta aag gga gat ata gtg gaa ctt aat aaa						331
Ser Ala Ala Leu Ala Ser Leu Lys Gly Asp Ile Val Glu Leu Asn Lys						
	25			30	35	
cgt ctc cag caa aca gag agg gaa cgg gac ctt ctg gaa aag aaa ttg						379
Arg Leu Gln Gln Thr Glu Arg Glu Arg Asp Leu Leu Glu Lys Lys Leu						
	40			45	50	
gcc aag gca cag tgc gag cag tcc cac ctc atg aga gag cat gag gat						427
Ala Lys Ala Gln Cys Glu Gln Ser His Leu Met Arg Glu His Glu Asp						
	55			60	65	
gtc cag gag cga acg acg ctt cgc tat gag gaa cgc atc aca gag ctc						475
Val Gln Glu Arg Thr Thr Leu Arg Tyr Glu Glu Arg Ile Thr Glu Leu						
	70			75	80	85
cac agc gtc att gcg gag ctc aac aag aag ata gac cgt ctg caa ggc						523
His Ser Val Ile Ala Glu Leu Asn Lys Lys Ile Asp Arg Leu Gln Gly						
	90			95	100	
acc acc atc agg gag gaa gat gag tac tca gaa ctg cga tca gaa ctc						571
Thr Thr Ile Arg Glu Glu Asp Glu Tyr Ser Glu Leu Arg Ser Glu Leu						
	105			110	115	
agc cag agc caa cac gag gtc aac gag gac tct cga agc atg gac caa						619
Ser Gln Ser Gln His Glu Val Asn Glu Asp Ser Arg Ser Met Asp Gln						
	120			125	130	
gac cag acc tct gtc tct atc ccc gaa aac cag tct acc atg gtt act						667
Asp Gln Thr Ser Val Ser Ile Pro Glu Asn Gln Ser Thr Met Val Thr						
	135			140	145	
gct gac atg gac aac tgc agt gac ctg aac tca gaa ctg cag agg gtc						715
Ala Asp Met Asp Asn Cys Ser Asp Leu Asn Ser Glu Leu Gln Arg Val						
	150			155	160	165
ctg aca ggg ctg gag aat gtt gtc tgc ggc agg aag aag agc agc tgc						763
Leu Thr Gly Leu Glu Asn Val Val Cys Gly Arg Lys Lys Ser Ser Cys						
	170			175	180	
agc ctc tcc gtg gcc gag gtg gac agg cac att gag cag ctc acc aca						811
Ser Leu Ser Val Ala Glu Val Asp Arg His Ile Glu Gln Leu Thr Thr						
	185			190	195	
gcc agc gag cac tgt gac ctg gct att aag aca gtc gag gag att gag						859
Ala Ser Glu His Cys Asp Leu Ala Ile Lys Thr Val Glu Glu Ile Glu						
	200			205	210	
ggg gtg ctt ggc cgg gac ctg tat ccc aac ctg gct gaa gag agg tct						907
Gly Val Leu Gly Arg Asp Leu Tyr Pro Asn Leu Ala Glu Glu Arg Ser						
	215			220	225	
cgg tgg gag aag gag ctg gct ggg ctg agg gaa gag aat gag agc ctg						955
Arg Trp Glu Lys Glu Leu Ala Gly Leu Arg Glu Glu Asn Glu Ser Leu						
	230			235	240	245
act gcc atg ctg tgc agc aaa gag gaa gaa ctg aac cgg act aag gcc						1003
Thr Ala Met Leu Cys Ser Lys Glu Glu Glu Leu Asn Arg Thr Lys Ala						
	250			255	260	

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acc atg aat gcc atc cgg gaa gag cgg gac cgg ctc cgg agg cgg gtc	1051
Thr Met Asn Ala Ile Arg Glu Glu Arg Asp Arg Leu Arg Arg Arg Val	
265 270 275	
aga gag ctt caa act cga cta cag agc gtg cag gcc aca ggt ccc tcc	1099
Arg Glu Leu Gln Thr Arg Leu Gln Ser Val Gln Ala Thr Gly Pro Ser	
280 285 290	
agc cct ggc cgc ctc act tcc acc aac cgc ccg att aac ccc agc act	1147
Ser Pro Gly Arg Leu Thr Ser Thr Asn Arg Pro Ile Asn Pro Ser Thr	
295 300 305	
ggg gag ctg agc aca agc agc agc agc aat gac att ccc atc gcc aag	1195
Gly Glu Leu Ser Thr Ser Ser Ser Ser Asn Asp Ile Pro Ile Ala Lys	
310 315 320 325	
att gct gag agg gtg aag cta tca aag aca agg tcc gaa tcg tca tca	1243
Ile Ala Glu Arg Val Lys Leu Ser Lys Thr Arg Ser Glu Ser Ser Ser	
330 335 340	
tct gat cgg cca gtc ctg ggc tca gaa atc agt agc ata ggg gta tcc	1291
Ser Asp Arg Pro Val Leu Gly Ser Glu Ile Ser Ser Ile Gly Val Ser	
345 350 355	
agc agt gtg gct gaa cac ctg gcc cac tca ctt cag gac tgc tcc aat	1339
Ser Ser Val Ala Glu His Leu Ala His Ser Leu Gln Asp Cys Ser Asn	
360 365 370	
atc caa gag att ttc caa aca ctc tac tca cac gga tct gcc atc tca	1387
Ile Gln Glu Ile Phe Gln Thr Leu Tyr Ser His Gly Ser Ala Ile Ser	
375 380 385	
gaa agc aag att aga gag ttt gag gtg gaa aca gaa cgg ctg aat agc	1435
Glu Ser Lys Ile Arg Glu Phe Glu Val Glu Thr Glu Arg Leu Asn Ser	
390 395 400 405	
cgg att gag cac ctc aaa tcc caa aat gac ctc ctg acc ata acc ttg	1483
Arg Ile Glu His Leu Lys Ser Gln Asn Asp Leu Leu Thr Ile Thr Leu	
410 415 420	
gag gaa tgt aaa agc aat gct gag agg atg agc atg ctg gtg gga aaa	1531
Glu Glu Cys Lys Ser Asn Ala Glu Arg Met Ser Met Leu Val Gly Lys	
425 430 435	
tac gaa tcc aat gcc aca gcg ctg agg ctg gcc ttg cag tac agc gag	1579
Tyr Glu Ser Asn Ala Thr Ala Leu Arg Leu Ala Leu Gln Tyr Ser Glu	
440 445 450	
cag tgc atc gaa gcc tac gaa ctc ctc ctg gcg ctg gca gag agt gag	1627
Gln Cys Ile Glu Ala Tyr Glu Leu Leu Leu Ala Leu Ala Glu Ser Glu	
455 460 465	
cag agc ctc atc ctg ggg cag ttc cga gcg gcg ggc gtg ggg tcc tcc	1675
Gln Ser Leu Ile Leu Gly Gln Phe Arg Ala Ala Gly Val Gly Ser Ser	
470 475 480 485	
cct gga gac cag tcg ggg gat gaa aac atc act cag atg ctc aag cga	1723
Pro Gly Asp Gln Ser Gly Asp Glu Asn Ile Thr Gln Met Leu Lys Arg	
490 495 500	
gct cat gac tgc cgg aag aca gct gag aac gct gcc aag gcc ctg ctc	1771
Ala His Asp Cys Arg Lys Thr Ala Glu Asn Ala Ala Lys Ala Leu Leu	
505 510 515	
atg aag ctg gac ggc agc tgt ggg gga gcc ttt gcc gtg gcc ggc tgc	1819
Met Lys Leu Asp Gly Ser Cys Gly Gly Ala Phe Ala Val Ala Gly Cys	
520 525 530	

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agc	gtg	cag	ccc	tgg	gag	agc	ctt	tcc	tcc	aac	agc	cac	acc	agc	aca	1867
Ser	Val	Gln	Pro	Trp	Glu	Ser	Leu	Ser	Ser	Asn	Ser	His	Thr	Ser	Thr	
	535					540					545					
acc	agc	tcc	aca	gcc	agt	agt	tgc	gac	acc	gag	ttc	act	aaa	gaa	gac	1915
Thr	Ser	Ser	Thr	Ala	Ser	Ser	Cys	Asp	Thr	Glu	Phe	Thr	Lys	Glu	Asp	
550					555					560					565	
gag	cag	agg	ctg	aag	gat	tat	atc	cag	cag	ctc	aag	aat	gac	agg	gct	1963
Glu	Gln	Arg	Leu	Lys	Asp	Tyr	Ile	Gln	Gln	Leu	Lys	Asn	Asp	Arg	Ala	
				570					575					580		
gcg	gtc	aag	ctg	acc	atg	ctg	gag	ctg	gaa	agc	atc	cac	atc	gat	cct	2011
Ala	Val	Lys	Leu	Thr	Met	Leu	Glu	Leu	Glu	Ser	Ile	His	Ile	Asp	Pro	
			585					590					595			
ctc	agc	tat	gac	gtc	aag	cct	cgg	gga	gac	agc	cag	agg	ctg	gat	ctg	2059
Leu	Ser	Tyr	Asp	Val	Lys	Pro	Arg	Gly	Asp	Ser	Gln	Arg	Leu	Asp	Leu	
		600					605					610				
gaa	aac	gca	gtg	ctt	atg	cag	gag	ctc	atg	gcc	atg	aag	gag	gag	atg	2107
Glu	Asn	Ala	Val	Leu	Met	Gln	Glu	Leu	Met	Ala	Met	Lys	Glu	Glu	Met	
	615					620					625					
gcc	gag	ttg	aag	gcc	cag	ctc	tac	cta	ctg	gag	aaa	gag	aag	aag	gcc	2155
Ala	Glu	Leu	Lys	Ala	Gln	Leu	Tyr	Leu	Leu	Glu	Lys	Glu	Lys	Lys	Ala	
630					635					640					645	
ctg	gag	ctg	aag	ctg	agc	acg	cgg	gag	gcc	cag	gag	cag	gcc	tac	ctg	2203
Leu	Glu	Leu	Lys	Leu	Ser	Thr	Arg	Glu	Ala	Gln	Glu	Gln	Ala	Tyr	Leu	
				650					655					660		
gtg	cac	att	gag	cac	ctg	aag	tcc	gag	gtg	gag	gag	cag	aag	gag	cag	2251
Val	His	Ile	Glu	His	Leu	Lys	Ser	Glu	Val	Glu	Glu	Gln	Lys	Glu	Gln	
			665					670					675			
cgg	atg	cga	tcc	ctc	agc	tcc	acc	agc	agc	ggc	agc	aaa	gat	aaa	cct	2299
Arg	Met	Arg	Ser	Leu	Ser	Ser	Thr	Ser	Ser	Gly	Ser	Lys	Asp	Lys	Pro	
		680					685					690				
ggc	aag	gag	tgt	gct	gat	gct	gcc	tcc	cca	gct	ctg	tcc	cta	gct	gaa	2347
Gly	Lys	Glu	Cys	Ala	Asp	Ala	Ala	Ser	Pro	Ala	Leu	Ser	Leu	Ala	Glu	
	695					700					705					
ctc	agg	aca	acg	tgc	agc	gag	aat	gag	ctg	gct	gcg	gag	ttc	acc	aac	2395
Leu	Arg	Thr	Thr	Cys	Ser	Glu	Asn	Glu	Leu	Ala	Ala	Glu	Phe	Thr	Asn	
710					715					720					725	
gcc	att	cgt	cga	gaa	aag	aag	ttg	aag	gcc	aga	gtt	caa	gag	ctg	gtg	2443
Ala	Ile	Arg	Arg	Glu	Lys	Lys	Leu	Lys	Ala	Arg	Val	Gln	Glu	Leu	Val	
				730					735					740		
agt	gcc	ttg	gag	aga	ctc	acc	aag	agc	agt	gaa	atc	cga	cat	cag	caa	2491
Ser	Ala	Leu	Glu	Arg	Leu	Thr	Lys	Ser	Ser	Glu	Ile	Arg	His	Gln	Gln	
			745					750					755			
tct	gca	gag	ttc	gtg	aat	gat	cta	aag	cgg	gcc	aac	agc	aac	ctg	gtg	2539
Ser	Ala	Glu	Phe	Val	Asn	Asp	Leu	Lys	Arg	Ala	Asn	Ser	Asn	Leu	Val	
		760					765					770				
gct	gcc	tat	gag	aaa	gca	aag	aaa	aag	cat	caa	aac	aaa	ctg	aag	aag	2587
Ala	Ala	Tyr	Glu	Lys	Ala	Lys	Lys	Lys	His	Gln	Asn	Lys	Leu	Lys	Lys	
	775					780					785					
tta	gag	tcg	cag	atg	atg	gcc	atg	gtg	gag	aga	cat	gag	acc	caa	gtg	2635
Leu	Glu	Ser	Gln	Met	Met	Ala	Met	Val	Glu	Arg	His	Glu	Thr	Gln	Val	
790					795					800					805	

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agg atg ctc aag caa aga ata gct ctg cta gag gag gag aac tcc agg	2683
Arg Met Leu Lys Gln Arg Ile Ala Leu Leu Glu Glu Glu Asn Ser Arg	
810 815 820	
cca cac acc aat gaa act tcg ctt taatcagcac tcacgcaccg gagttctgcc	2737
Pro His Thr Asn Glu Thr Ser Leu	
825	
catgggaagt aaactgcagc aggccactgg ggacagaagg gcccattgtac ttgttgggag	2797
gaggaggaaa ggggaaggctg gcaggtaggt cggcacttgg acaatggagt gcccgaactc	2857
aacccttggg gtgactggcc atggtgacat tgtggactgt atccagagggt gcccgtctct	2917
ccctcctggg cccacaacag cgtgtaaaca catgttctgt gcctgctcag cagagcctcg	2977
tttctgcttt cagcactcac tctccccctc ctcttctggt ctggcggctg tgcattcagt	3037
ggatcccgaga catttgcttc tgtaagattt tccattgtat cctctttttg gtagatgctg	3097
ggctcatctt ctagaatctc gtttctcctc tttcctcctg cttcatggga aaacagacct	3157
gtgtgtgcct ccagcattta aaaggactgc tgatttgctt actacagcaa ggctttgggt	3217
tccaagtccc ggggtctcaac ttaagatag aggcggccat aagagggtgat ctctgggagt	3277
tatagggtcat ggggaagagcg tagacagggt ttacttacag tcccagatac actaaagtta	3337
caaacagacc accaccagga ctgtgcctga acaattttgt attgagagaa taaaaacttc	3397
cttcaatctt cattttggag gcagggctgg gaaggagcg ctctcttgat tctgggattt	3457
ctccctctca gtggagcctt attaatatcc aagacttaga gctgggaatc tttttgatac	3517
ctgtagtgga actaaaattc tgtcaggggt ttcttcaaga gctgagaaac attattagca	3577
cttcccgcgc cagggcacta cataattgct gttctgctga atcaaattctc ttccacatgg	3637
gtgcatttgt agctctggac ctgtctctac ctaaggacaa gacactgagg agatactgaa	3697
cattttgcaa aacttatcac gcctacttaa gagtgctgtg taacccccag ttcaagactt	3757
agctcctggt gtcattgacgg ggacagagtg agggaatggt agttaaggct tcttttttgc	3817
ccccagatac atggtgatgg ttagcatatg gtgcttaaaa ggttaaattt caagcaaaat	3877
gcttacaggg ctaggcagta ccaaagtaac tgaattattt caggaagggtc ttcaatctta	3937
aaacaaattc attattcttt ttcagtttta cctcttctct ctcagttcta cactgataca	3997
cttgaaggac catttactgt ttttttctgt agcaccagag aatccatcca aagtcccta	4057
tgaaaaatgt gttccattgc catagctgac tacaaattaa agttgaggag gtttctgcat	4117
agagtcttta tgtccataag ctacgggtag gtctattttc agagcatgat acaaattcca	4177
cagg	4181

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 <213> homo sapiens

<400> 4

Met Asn Ser Gly Val Ala Met Lys Tyr Gly Asn Asp Ser Ser Ala Glu

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1 5 10 15

Leu Ser Glu Leu His Ser Ala Ala Leu Ala Ser Leu Lys Gly Asp Ile  
20 25 30

Val Glu Leu Asn Lys Arg Leu Gln Gln Thr Glu Arg Glu Arg Asp Leu  
35 40 45

Leu Glu Lys Lys Leu Ala Lys Ala Gln Cys Glu Gln Ser His Leu Met  
50 55 60

Arg Glu His Glu Asp Val Gln Glu Arg Thr Thr Leu Arg Tyr Glu Glu  
65 70 75 80

Arg Ile Thr Glu Leu His Ser Val Ile Ala Glu Leu Asn Lys Lys Ile  
85 90 95

Asp Arg Leu Gln Gly Thr Thr Ile Arg Glu Glu Asp Glu Tyr Ser Glu  
100 105 110

Leu Arg Ser Glu Leu Ser Gln Ser Gln His Glu Val Asn Glu Asp Ser  
115 120 125

Arg Ser Met Asp Gln Asp Gln Thr Ser Val Ser Ile Pro Glu Asn Gln  
130 135 140

Ser Thr Met Val Thr Ala Asp Met Asp Asn Cys Ser Asp Leu Asn Ser  
145 150 155 160

Glu Leu Gln Arg Val Leu Thr Gly Leu Glu Asn Val Val Cys Gly Arg  
165 170 175

Lys Lys Ser Ser Cys Ser Leu Ser Val Ala Glu Val Asp Arg His Ile  
180 185 190

Glu Gln Leu Thr Thr Ala Ser Glu His Cys Asp Leu Ala Ile Lys Thr  
195 200 205

Val Glu Glu Ile Glu Gly Val Leu Gly Arg Asp Leu Tyr Pro Asn Leu  
210 215 220

Ala Glu Glu Arg Ser Arg Trp Glu Lys Glu Leu Ala Gly Leu Arg Glu  
225 230 235 240

Glu Asn Glu Ser Leu Thr Ala Met Leu Cys Ser Lys Glu Glu Glu Leu  
245 250 255

Asn Arg Thr Lys Ala Thr Met Asn Ala Ile Arg Glu Glu Arg Asp Arg  
260 265 270

Leu Arg Arg Arg Val Arg Glu Leu Gln Thr Arg Leu Gln Ser Val Gln

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275

280

285

Ala Thr Gly Pro Ser Ser Pro Gly Arg Leu Thr Ser Thr Asn Arg Pro  
 290 295 300

Ile Asn Pro Ser Thr Gly Glu Leu Ser Thr Ser Ser Ser Ser Asn Asp  
 305 310 315 320

Ile Pro Ile Ala Lys Ile Ala Glu Arg Val Lys Leu Ser Lys Thr Arg  
 325 330 335

Ser Glu Ser Ser Ser Ser Asp Arg Pro Val Leu Gly Ser Glu Ile Ser  
 340 345 350

Ser Ile Gly Val Ser Ser Ser Val Ala Glu His Leu Ala His Ser Leu  
 355 360 365

Gln Asp Cys Ser Asn Ile Gln Glu Ile Phe Gln Thr Leu Tyr Ser His  
 370 375 380

Gly Ser Ala Ile Ser Glu Ser Lys Ile Arg Glu Phe Glu Val Glu Thr  
 385 390 395 400

Glu Arg Leu Asn Ser Arg Ile Glu His Leu Lys Ser Gln Asn Asp Leu  
 405 410 415

Leu Thr Ile Thr Leu Glu Glu Cys Lys Ser Asn Ala Glu Arg Met Ser  
 420 425 430

Met Leu Val Gly Lys Tyr Glu Ser Asn Ala Thr Ala Leu Arg Leu Ala  
 435 440 445

Leu Gln Tyr Ser Glu Gln Cys Ile Glu Ala Tyr Glu Leu Leu Leu Ala  
 450 455 460

Leu Ala Glu Ser Glu Gln Ser Leu Ile Leu Gly Gln Phe Arg Ala Ala  
 465 470 475 480

Gly Val Gly Ser Ser Pro Gly Asp Gln Ser Gly Asp Glu Asn Ile Thr  
 485 490 495

Gln Met Leu Lys Arg Ala His Asp Cys Arg Lys Thr Ala Glu Asn Ala  
 500 505 510

Ala Lys Ala Leu Leu Met Lys Leu Asp Gly Ser Cys Gly Gly Ala Phe  
 515 520 525

Ala Val Ala Gly Cys Ser Val Gln Pro Trp Glu Ser Leu Ser Ser Asn  
 530 535 540

Ser His Thr Ser Thr Thr Ser Ser Thr Ala Ser Ser Cys Asp Thr Glu

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545 550 555 560

Phe Thr Lys Glu Asp Glu Gln Arg Leu Lys Asp Tyr Ile Gln Gln Leu  
565 570 575

Lys Asn Asp Arg Ala Ala Val Lys Leu Thr Met Leu Glu Leu Glu Ser  
580 585 590

Ile His Ile Asp Pro Leu Ser Tyr Asp Val Lys Pro Arg Gly Asp Ser  
595 600 605

Gln Arg Leu Asp Leu Glu Asn Ala Val Leu Met Gln Glu Leu Met Ala  
610 615 620

Met Lys Glu Glu Met Ala Glu Leu Lys Ala Gln Leu Tyr Leu Leu Glu  
625 630 635 640

Lys Glu Lys Lys Ala Leu Glu Leu Lys Leu Ser Thr Arg Glu Ala Gln  
645 650 655

Glu Gln Ala Tyr Leu Val His Ile Glu His Leu Lys Ser Glu Val Glu  
660 665 670

Glu Gln Lys Glu Gln Arg Met Arg Ser Leu Ser Ser Thr Ser Ser Gly  
675 680 685

Ser Lys Asp Lys Pro Gly Lys Glu Cys Ala Asp Ala Ala Ser Pro Ala  
690 695 700

Leu Ser Leu Ala Glu Leu Arg Thr Thr Cys Ser Glu Asn Glu Leu Ala  
705 710 715 720

Ala Glu Phe Thr Asn Ala Ile Arg Arg Glu Lys Lys Leu Lys Ala Arg  
725 730 735

Val Gln Glu Leu Val Ser Ala Leu Glu Arg Leu Thr Lys Ser Ser Glu  
740 745 750

Ile Arg His Gln Gln Ser Ala Glu Phe Val Asn Asp Leu Lys Arg Ala  
755 760 765

Asn Ser Asn Leu Val Ala Ala Tyr Glu Lys Ala Lys Lys Lys His Gln  
770 775 780

Asn Lys Leu Lys Lys Leu Glu Ser Gln Met Met Ala Met Val Glu Arg  
785 790 795 800

His Glu Thr Gln Val Arg Met Leu Lys Gln Arg Ile Ala Leu Leu Glu  
805 810 815

Glu Glu Asn Ser Arg Pro His Thr Asn Glu Thr Ser Leu

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agcggcagcg acgcggctaa aagcgaaggg gcgagtgcga gtcccctgag ctgtacgaac      120
gcggtcgcc atg gac cgc cca gat gag ggg cct ccg gcc aag acc cgc cgc      171
          Met Asp Arg Pro Asp Glu Gly Pro Pro Ala Lys Thr Arg Arg
          1          5          10

ctg agc agc tcc gag tct cca cag cgc gac ccg ccc ccg ccg ccg ccg      219
Leu Ser Ser Ser Glu Ser Pro Gln Arg Asp Pro Pro Pro Pro Pro Pro
15          20          25          30

ccg ccg ccg ctc ctc cga ctg ccg ctg cct cca ccc cag cag cgc ccg      267
Pro Pro Pro Leu Leu Arg Leu Pro Leu Pro Pro Pro Gln Gln Arg Pro
35          40          45

agg ctc cag gag gaa acg gag gcg gca cag gtg ctg gcc gat atg agg      315
Arg Leu Gln Glu Glu Thr Glu Ala Ala Gln Val Leu Ala Asp Met Arg
50          55          60

ggg gtg gga ctg ggc ccc gcg ctg ccc ccg ccg cct ccc tat gtc att      363
Gly Val Gly Leu Gly Pro Ala Leu Pro Pro Pro Pro Pro Tyr Val Ile
65          70          75

ctc gag gag ggg ggg atc cgc gca tac ttc acg ctc ggt gct gag tgt      411
Leu Glu Glu Gly Gly Ile Arg Ala Tyr Phe Thr Leu Gly Ala Glu Cys
80          85          90

ccc ggc tgg gat tct acc atc gag tcg ggg tat ggg gag gcg ccc ccg      459
Pro Gly Trp Asp Ser Thr Ile Glu Ser Gly Tyr Gly Glu Ala Pro Pro
95          100          105          110

ccc acg gag agc ctg gaa gca ctc ccc act cct gag gcc tcg ggg ggg      507
Pro Thr Glu Ser Leu Glu Ala Leu Pro Thr Pro Glu Ala Ser Gly Gly
115          120          125

agc ctg gaa atc gat ttt cag gtt gta cag tcg agc agt ttt ggt gga      555
Ser Leu Glu Ile Asp Phe Gln Val Val Gln Ser Ser Ser Phe Gly Gly
130          135          140

gag ggg gcc cta gaa acc tgt agc gca gtg ggg tgg gcg ccc cag agg      603
Glu Gly Ala Leu Glu Thr Cys Ser Ala Val Gly Trp Ala Pro Gln Arg
145          150          155

tta gtt gac ccg aag agc aag gaa gag gcg atc atc ata gtg gag gat      651
Leu Val Asp Pro Lys Ser Lys Glu Glu Ala Ile Ile Ile Val Glu Asp
160          165          170

gag gat gag gat gag cgg gag agt atg agg agc agc agg agg cgg cgg      699
Glu Asp Glu Asp Glu Arg Glu Ser Met Arg Ser Ser Arg Arg Arg Arg
175          180          185          190

cgg cgg cgg agg agg aag cag agg aag gtg aag agg gaa agc aga gag      747
Arg Arg Arg Arg Arg Lys Gln Arg Lys Val Lys Arg Glu Ser Arg Glu

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122257 sequence listing May 10 2006.ST25.txt  
195 200 205

aga	aat	gcc	gag	agg	atg	gag	agc	atc	ctg	cag	gca	ctg	gag	gat	att	795
Arg	Asn	Ala	Glu	Arg	Met	Glu	Ser	Ile	Leu	Gln	Ala	Leu	Glu	Asp	Ile	
			210					215					220			
cag	ctg	gat	ctg	gag	gca	gtg	aac	atc	aag	gca	ggc	aaa	gcc	ttc	ctg	843
Gln	Leu	Asp	Leu	Glu	Ala	Val	Asn	Ile	Lys	Ala	Gly	Lys	Ala	Phe	Leu	
		225					230					235				
cgt	ctc	aag	cgc	aag	ttc	atc	cag	atg	cga	aga	ccc	ttc	ctg	gag	cgc	891
Arg	Leu	Lys	Arg	Lys	Phe	Ile	Gln	Met	Arg	Arg	Pro	Phe	Leu	Glu	Arg	
	240					245					250					
aga	gac	ctc	atc	atc	cag	cat	atc	cca	ggc	ttc	tgg	gtc	aaa	gca	ttc	939
Arg	Asp	Leu	Ile	Ile	Gln	His	Ile	Pro	Gly	Phe	Trp	Val	Lys	Ala	Phe	
255					260					265					270	
ctc	aac	cac	ccc	aga	att	tca	att	ttg	atc	aac	cga	cgt	gat	gaa	gac	987
Leu	Asn	His	Pro	Arg	Ile	Ser	Ile	Leu	Ile	Asn	Arg	Arg	Asp	Glu	Asp	
				275					280					285		
att	ttc	cgc	tac	ttg	acc	aat	ctg	cag	gta	cag	gat	ctc	aga	cat	atc	1035
Ile	Phe	Arg	Tyr	Leu	Thr	Asn	Leu	Gln	Val	Gln	Asp	Leu	Arg	His	Ile	
			290					295					300			
tcc	atg	ggc	tac	aaa	atg	aag	ctg	tac	ttc	cag	act	aac	ccc	tac	ttc	1083
Ser	Met	Gly	Tyr	Lys	Met	Lys	Leu	Tyr	Phe	Gln	Thr	Asn	Pro	Tyr	Phe	
		305					310					315				
aca	aac	atg	gtg	att	gtc	aag	gag	ttc	cag	cgc	aac	cgc	tca	ggc	cgg	1131
Thr	Asn	Met	Val	Ile	Val	Lys	Glu	Phe	Gln	Arg	Asn	Arg	Ser	Gly	Arg	
	320					325					330					
ctg	gtg	tct	cac	tca	acc	cca	atc	cgc	tgg	cac	cgg	ggc	cag	gaa	ccc	1179
Leu	Val	Ser	His	Ser	Thr	Pro	Ile	Arg	Trp	His	Arg	Gly	Gln	Glu	Pro	
335					340					345					350	
cag	gcc	cgt	cgt	cac	ggg	aac	cag	gat	gcg	agc	cac	agc	ttt	ttc	agc	1227
Gln	Ala	Arg	Arg	His	Gly	Asn	Gln	Asp	Ala	Ser	His	Ser	Phe	Phe	Ser	
				355					360					365		
tgg	ttc	tca	aac	cat	agc	ctc	cca	gag	gct	gac	agg	att	gct	gag	att	1275
Trp	Phe	Ser	Asn	His	Ser	Leu	Pro	Glu	Ala	Asp	Arg	Ile	Ala	Glu	Ile	
			370					375					380			
atc	aag	aat	gat	ctg	tgg	gtt	aac	cct	cta	cgc	tac	tac	ctg	aga	gaa	1323
Ile	Lys	Asn	Asp	Leu	Trp	Val	Asn	Pro	Leu	Arg	Tyr	Tyr	Leu	Arg	Glu	
		385					390					395				
agg	ggc	tcc	agg	ata	aag	aga	aag	aag	caa	gaa	atg	aag	aaa	cgt	aaa	1371
Arg	Gly	Ser	Arg	Ile	Lys	Arg	Lys	Lys	Gln	Glu	Met	Lys	Lys	Arg	Lys	
	400					405					410					
acc	agg	ggc	aga	tgt	gag	gtg	gtg	atc	atg	gaa	gac	gcc	cct	gac	tat	1419
Thr	Arg	Gly	Arg	Cys	Glu	Val	Val	Ile	Met	Glu	Asp	Ala	Pro	Asp	Tyr	
415					420					425					430	
tat	gca	gtg	gaa	gac	att	ttc	agc	gag	atc	tca	gac	att	gat	gag	aca	1467
Tyr	Ala	Val	Glu	Asp	Ile	Phe	Ser	Glu	Ile	Ser	Asp	Ile	Asp	Glu	Thr	
				435					440					445		
att	cat	gac	atc	aag	atc	tct	gac	ttc	atg	gag	acc	acc	gac	tac	ttc	1515
Ile	His	Asp	Ile	Lys	Ile	Ser	Asp	Phe	Met	Glu	Thr	Thr	Asp	Tyr	Phe	
			450					455					460			
gag	acc	act	gac	aat	gag	ata	act	gac	atc	aat	gag	aac	atc	tgc	gac	1563
Glu	Thr	Thr	Asp	Asn	Glu	Ile	Thr	Asp	Ile	Asn	Glu	Asn	Ile	Cys	Asp	

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465		470		475													
agc	gag	aat	cct	gac	cac	aat	gag	gtc	ccc	aac	aac	gag	acc	act	gat		1611
Ser	Glu	Asn	Pro	Asp	His	Asn	Glu	Val	Pro	Asn	Asn	Glu	Thr	Thr	Asp		
	480					485					490						
aac	aac	gag	agt	gct	gat	gac	cac	gaa	acc	act	gac	aac	aat	gag	agt		1659
Asn	Asn	Glu	Ser	Ala	Asp	Asp	His	Glu	Thr	Thr	Asp	Asn	Asn	Glu	Ser		
495					500					505					510		
gca	gat	gac	aac	aac	gag	aat	cct	gaa	gac	aat	aac	aag	aac	act	gat		1707
Ala	Asp	Asp	Asn	Asn	Glu	Asn	Pro	Glu	Asp	Asn	Asn	Lys	Asn	Thr	Asp		
				515					520					525			
gac	aac	gaa	gag	aac	cct	aac	aac	aac	gag	aac	act	tac	ggc	aac	aac		1755
Asp	Asn	Glu	Glu	Asn	Pro	Asn	Asn	Asn	Glu	Asn	Thr	Tyr	Gly	Asn	Asn		
			530					535					540				
ttc	ttc	aaa	ggg	ggc	ttc	tgg	ggc	agc	cat	ggc	aac	aac	cag	gac	agc		1803
Phe	Phe	Lys	Gly	Gly	Phe	Trp	Gly	Ser	His	Gly	Asn	Asn	Gln	Asp	Ser		
		545					550					555					
agc	gac	agt	gac	aat	gaa	gca	gat	gag	gcc	agt	gat	gat	gaa	gat	aat		1851
Ser	Asp	Ser	Asp	Asn	Glu	Ala	Asp	Glu	Ala	Ser	Asp	Asp	Glu	Asp	Asn		
	560					565					570						
gat	ggc	aac	gaa	ggg	gac	aat	gag	ggc	agt	gat	gat	gat	ggc	aat	gaa		1899
Asp	Gly	Asn	Glu	Gly	Asp	Asn	Glu	Gly	Ser	Asp	Asp	Asp	Gly	Asn	Glu		
575					580					585					590		
ggg	gac	aat	gaa	ggc	agc	gat	gat	gac	gac	aga	gac	att	gag	tac	tat		1947
Gly	Asp	Asn	Glu	Gly	Ser	Asp	Asp	Asp	Asp	Arg	Asp	Ile	Glu	Tyr	Tyr		
				595					600					605			
gag	aaa	gtt	att	gaa	gac	ttt	gac	aag	gat	cag	gct	gac	tac	gag	gac		1995
Glu	Lys	Val	Ile	Glu	Asp	Phe	Asp	Lys	Asp	Gln	Ala	Asp	Tyr	Glu	Asp		
			610					615					620				
gtg	ata	gag	atc	atc	tca	gac	gaa	tca	gtg	gaa	gaa	gag	ggc	att	gag		2043
Val	Ile	Glu	Ile	Ile	Ser	Asp	Glu	Ser	Val	Glu	Glu	Glu	Gly	Ile	Glu		
		625					630					635					
gaa	ggc	atc	cag	caa	gat	gag	gac	atc	tat	gag	gaa	gga	aac	tat	gag		2091
Glu	Gly	Ile	Gln	Gln	Asp	Glu	Asp	Ile	Tyr	Glu	Glu	Gly	Asn	Tyr	Glu		
	640					645					650						
gag	gaa	gga	agt	gaa	gat	gtc	tgg	gaa	gaa	ggg	gaa	gat	tcg	gac	gac		2139
Glu	Glu	Gly	Ser	Glu	Asp	Val	Trp	Glu	Glu	Gly	Glu	Asp	Ser	Asp	Asp		
655					660					665					670		
tct	gac	cta	gag	gat	gtg	ctt	cag	gtc	cca	aac	ggg	tgg	gcc	aat	ccg		2187
Ser	Asp	Leu	Glu	Asp	Val	Leu	Gln	Val	Pro	Asn	Gly	Trp	Ala	Asn	Pro		
				675					680					685			
ggg	aag	agg	ggg	aaa	acc	gga	taagggtttt	cccccttttg	ggatcacctc								2238
Gly	Lys	Arg	Gly	Lys	Thr	Gly											
			690														
tctgtatccc	ccaccacta	tcccatttgc	cctcctcctc	agctagggcc	acgcggcccc												2298
acattgcact	tctggggggg	gaccgacttc	gtacacgggt	ttaaagttta	tttttatggg												2358
ttagtcattg	cagagttctt	attttggggg	gagggaaagg	gggctagtcc	ccttcttttg												2418
gccctccgcc	cccgcaggct	tctgtgtgct	gctaactgta	tttattgtga	tgccttggtc												2478
agggccccctc	taccacttc	tcccagtcag	ttgtggcccc	agccccctctc	cctgtgctgt												2538

122257 sequence listing May 10 2006.ST25.txt  
 gtggagtgga caccctgacc cccgaagcgg ggagggccgc tgtggccttc gtcacagccg 2598  
 cgcagtcccc atggaggcgc tgctgccacc ttcctctccc aagttctttc tccatccctc 2658  
 tcctcttccc gccgcgccgc tagcccgctt cgggtgtctat gcaaggccgc ttcgccattg 2718  
 cgggtattctt tgcggtattc ttgtccccgt cccccagaag gctcgcctct ccccgtaggac 2778  
 cctgttaatc ccaataaaaat tctgagcaag ttcaaaaaaa aaaaaaaaaa aa 2830

<210> 6  
 <211> 693  
 <212> PRT  
 <213> homo sapiens

<400> 6

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 1 5 10 15

Ser Ser Glu Ser Pro Gln Arg Asp Pro Pro Pro Pro Pro Pro Pro  
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Pro Leu Leu Arg Leu Pro Leu Pro Pro Gln Gln Arg Pro Arg Leu  
 35 40 45

Gln Glu Glu Thr Glu Ala Ala Gln Val Leu Ala Asp Met Arg Gly Val  
 50 55 60

Gly Leu Gly Pro Ala Leu Pro Pro Pro Pro Pro Tyr Val Ile Leu Glu  
 65 70 75 80

Glu Gly Gly Ile Arg Ala Tyr Phe Thr Leu Gly Ala Glu Cys Pro Gly  
 85 90 95

Trp Asp Ser Thr Ile Glu Ser Gly Tyr Gly Glu Ala Pro Pro Pro Thr  
 100 105 110

Glu Ser Leu Glu Ala Leu Pro Thr Pro Glu Ala Ser Gly Gly Ser Leu  
 115 120 125

Glu Ile Asp Phe Gln Val Val Gln Ser Ser Ser Phe Gly Gly Glu Gly  
 130 135 140

Ala Leu Glu Thr Cys Ser Ala Val Gly Trp Ala Pro Gln Arg Leu Val  
 145 150 155 160

Asp Pro Lys Ser Lys Glu Glu Ala Ile Ile Ile Val Glu Asp Glu Asp  
 165 170 175

Glu Asp Glu Arg Glu Ser Met Arg Ser Ser Arg Arg Arg Arg Arg  
 180 185 190

Arg Arg Arg Lys Gln Arg Lys Val Lys Arg Glu Ser Arg Glu Arg Asn  
 195 200 205

122257 sequence listing May 10 2006.ST25.txt

Ala Glu Arg Met Glu Ser Ile Leu Gln Ala Leu Glu Asp Ile Gln Leu  
210 215 220

Asp Leu Glu Ala Val Asn Ile Lys Ala Gly Lys Ala Phe Leu Arg Leu  
225 230 235 240

Lys Arg Lys Phe Ile Gln Met Arg Arg Pro Phe Leu Glu Arg Arg Asp  
245 250 255

Leu Ile Ile Gln His Ile Pro Gly Phe Trp Val Lys Ala Phe Leu Asn  
260 265 270

His Pro Arg Ile Ser Ile Leu Ile Asn Arg Arg Asp Glu Asp Ile Phe  
275 280 285

Arg Tyr Leu Thr Asn Leu Gln Val Gln Asp Leu Arg His Ile Ser Met  
290 295 300

Gly Tyr Lys Met Lys Leu Tyr Phe Gln Thr Asn Pro Tyr Phe Thr Asn  
305 310 315 320

Met Val Ile Val Lys Glu Phe Gln Arg Asn Arg Ser Gly Arg Leu Val  
325 330 335

Ser His Ser Thr Pro Ile Arg Trp His Arg Gly Gln Glu Pro Gln Ala  
340 345 350

Arg Arg His Gly Asn Gln Asp Ala Ser His Ser Phe Phe Ser Trp Phe  
355 360 365

Ser Asn His Ser Leu Pro Glu Ala Asp Arg Ile Ala Glu Ile Ile Lys  
370 375 380

Asn Asp Leu Trp Val Asn Pro Leu Arg Tyr Tyr Leu Arg Glu Arg Gly  
385 390 395 400

Ser Arg Ile Lys Arg Lys Lys Gln Glu Met Lys Lys Arg Lys Thr Arg  
405 410 415

Gly Arg Cys Glu Val Val Ile Met Glu Asp Ala Pro Asp Tyr Tyr Ala  
420 425 430

Val Glu Asp Ile Phe Ser Glu Ile Ser Asp Ile Asp Glu Thr Ile His  
435 440 445

Asp Ile Lys Ile Ser Asp Phe Met Glu Thr Thr Asp Tyr Phe Glu Thr  
450 455 460

Thr Asp Asn Glu Ile Thr Asp Ile Asn Glu Asn Ile Cys Asp Ser Glu  
465 470 475 480

122257 sequence listing May 10 2006.ST25.txt

Asn Pro Asp His Asn Glu Val Pro Asn Asn Glu Thr Thr Asp Asn Asn  
485 490 495

Glu Ser Ala Asp Asp His Glu Thr Thr Asp Asn Asn Glu Ser Ala Asp  
500 505 510

Asp Asn Asn Glu Asn Pro Glu Asp Asn Asn Lys Asn Thr Asp Asp Asn  
515 520 525

Glu Glu Asn Pro Asn Asn Asn Glu Asn Thr Tyr Gly Asn Asn Phe Phe  
530 535 540

Lys Gly Gly Phe Trp Gly Ser His Gly Asn Asn Gln Asp Ser Ser Asp  
545 550 555 560

Ser Asp Asn Glu Ala Asp Glu Ala Ser Asp Asp Glu Asp Asn Asp Gly  
565 570 575

Asn Glu Gly Asp Asn Glu Gly Ser Asp Asp Asp Gly Asn Glu Gly Asp  
580 585 590

Asn Glu Gly Ser Asp Asp Asp Asp Arg Asp Ile Glu Tyr Tyr Glu Lys  
595 600 605

Val Ile Glu Asp Phe Asp Lys Asp Gln Ala Asp Tyr Glu Asp Val Ile  
610 615 620

Glu Ile Ile Ser Asp Glu Ser Val Glu Glu Glu Gly Ile Glu Glu Gly  
625 630 635 640

Ile Gln Gln Asp Glu Asp Ile Tyr Glu Glu Gly Asn Tyr Glu Glu Glu  
645 650 655

Gly Ser Glu Asp Val Trp Glu Glu Gly Glu Asp Ser Asp Asp Ser Asp  
660 665 670

Leu Glu Asp Val Leu Gln Val Pro Asn Gly Trp Ala Asn Pro Gly Lys  
675 680 685

Arg Gly Lys Thr Gly  
690

<210> 7  
<211> 2632  
<212> DNA  
<213> homo sapiens

<220>  
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<222> (931)..(1611)

## 122257 sequence listing May 10 2006.ST25.txt

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cgcgtcccag ccctgcccag cccgcgcccga gccatgcgcg ccgcctgctg agtccgggcg      180
ccgcacgctg agccctccgc ccgcgagccg cgctcagctc gggggtgatt agttgctttt      240
tgttgttttt taatttgggc cgcggggagg gggaggaggg gcaggtgctg caggctcccc      300
cccctccccg cctcggggcca gccgcggcgg cgcgactcgg gctccggacc cgggcactgc      360
tggcggctgg agcggagcgc accgcggcgg tggtgcccag agcggagcgc agctccctgc      420
cccgcccctc cccctcggcc tcgcggcgac ggcggcggtg gcggcttgga cgactcggag      480
agccgagtga agacatttcc acctggacac ctgacctatgt gcctgccctg agcagcgagg      540
cccaccaggc atctctgttg tgggcagcag ggccagggtcc tgggtctgtg accctcggca      600
gttggcaggc tccctctgca gtgggggtctg ggcctcggcc ccacctatgtc gagcctcggc      660
ggtggctccc aggatgccgg cggcagtagc agcagcagca ccaatggcag cggtggcagt      720
ggcagcagtg gcccaaaggc aggagcagca gacaagagtg cagtgggtggc tgccgccgca      780
ccagcctcag tggcagatga cacaccaccc cccgagcgtc ggaacaagag cggtatcatc      840
agtgagcccc tcaacaagag cctgcgccgc tcccgccgcg tctcccacta ctcttctttt      900
ggcagcagtg gtggtagtgg cggtggcagc atg atg ggc gga gag tct gct gac      954
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                               Met Met Gly Gly Glu Ser Ala Asp

aag gcc act gcg gct gca gcc gct gcc tcc ctg ttg gcc aat ggg cat      1002
Lys Ala Thr Ala Ala Ala Ala Val Ala Ser Leu Leu Ala Asn Gly His
    10                               15                               20

gac ctg gcg gcg gcc atg gcg gtg gac aaa agc aac cct acc tca aag      1050
Asp Leu Ala Ala Ala Met Ala Val Asp Lys Ser Asn Pro Thr Ser Lys
    25                               30                               35                               40

cac aaa agt ggt gct gtg gcc agc ctg ctg agc aag gca gag cgg gcc      1098
His Lys Ser Gly Ala Val Ala Ser Leu Leu Ser Lys Ala Glu Arg Ala
                               45                               50                               55

acg gag ctg gca gcc gag gga cag ctg acg ctg cag cag ttt gcg cag      1146
Thr Glu Leu Ala Ala Glu Gly Gln Leu Thr Leu Gln Gln Phe Ala Gln
                               60                               65                               70

tcc aca gag atg ctg aag cgc gtg gtg cag gag cat ctc ccg ctg atg      1194
Ser Thr Glu Met Leu Lys Arg Val Val Gln Glu His Leu Pro Leu Met
                               75                               80                               85

agc gag gcg ggt gct ggc ctg cct gac atg gag gct gtg gca ggt gcc      1242
Ser Glu Ala Gly Ala Gly Leu Pro Asp Met Glu Ala Val Ala Gly Ala
    90                               95                               100

gaa gcc ctc aat ggc cag tcc gac ttc ccc tac ctg ggc gct ttc ccc      1290
Glu Ala Leu Asn Gly Gln Ser Asp Phe Pro Tyr Leu Gly Ala Phe Pro
    105                               110                               115                               120

atc aac cca ggc ctc ttc att atg acc ccg gca ggt gtg ttc ctg gcc      1338
Ile Asn Pro Gly Leu Phe Ile Met Thr Pro Ala Gly Val Phe Leu Ala
                               125                               130                               135

gag agc gcg ctg cac atg gcg ggc ctg gct gag tac ccc atg cag gga      1386

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122257 sequence listing May 10 2006.ST25.txt

Glu	Ser	Ala	Leu	His	Met	Ala	Gly	Leu	Ala	Glu	Tyr	Pro	Met	Gln	Gly	
			140					145					150			
gag	ctg	gcc	tct	gcc	atc	agc	tcc	ggc	aag	aag	aag	cgg	aaa	cgc	tgc	1434
Glu	Leu	Ala	Ser	Ala	Ile	Ser	Ser	Gly	Lys	Lys	Lys	Arg	Lys	Arg	Cys	
		155					160					165				
ggc	atg	tgc	gcg	ccc	tgc	cgg	cgg	cgc	atc	aac	tgc	gag	cag	tgc	agc	1482
Gly	Met	Cys	Ala	Pro	Cys	Arg	Arg	Arg	Ile	Asn	Cys	Glu	Gln	Cys	Ser	
	170					175					180					
agt	tgt	agg	aat	cga	aag	act	ggc	cat	cag	att	tgc	aaa	ttc	aga	aaa	1530
Ser	Cys	Arg	Asn	Arg	Lys	Thr	Gly	His	Gln	Ile	Cys	Lys	Phe	Arg	Lys	
185					190					195					200	
tgt	gag	gaa	ctc	aaa	aag	aag	cct	tcc	gct	gct	ctg	gag	aag	gtg	atg	1578
Cys	Glu	Glu	Leu	Lys	Lys	Lys	Pro	Ser	Ala	Ala	Leu	Glu	Lys	Val	Met	
			205						210					215		
ctt	ccg	acg	gga	gcc	gcc	ttc	cgg	tgg	ttt	cag	tgacggcggc	ggaacccaaa				1631
Leu	Pro	Thr	Gly	Ala	Ala	Phe	Arg	Trp	Phe	Gln						
			220					225								
gctgccctct	ccgtgcaatg	tcactgctcg	tgtggtctcc	agcaagggat	tcgggccaag											1691
acaaacggat	gcacccgtct	ttagaaccaa	aaatattctc	tcacagattt	cattcctgtt											1751
tttatatata	tattttttgt	tgctgtttta	acatctccac	gtccctagca	taaaaagaaa											1811
aagaaaaaaa	tttaaactgc	tttttcggaa	gaacaacaac	aaaaaagagg	taaagacgaa											1871
tctataaagt	accgagactt	cctgggcaaa	gaatggacaa	tcagtttcct	tcctgtgtcg											1931
atgtcgaagt	tgtctgtgca	ggagatgcag	tttttgtgta	gagaatgtaa	attttctgta											1991
accttttgaa	atctagttac	taataagcac	tactgtaatt	tagcacagtt	taactccacc											2051
ctcattttaa	cttcctttga	ttctttccga	ccatgaaata	gtgcatagtt	tgccctggaga											2111
atccactcac	gttcataaag	agaatgttga	tggcgccgtg	tagaagccgc	tctgtatcca											2171
tccacgcgtg	cagagctgcc	agcagggagc	tcacagaagg	ggagggagca	ccaggccagc											2231
tgagctgcac	ccacagtccc	gagactggga	tccccaccc	caacagtgat	tttggaaaaa											2291
aaaatgaaag	ttctgttcgt	ttatccattg	cgatctgggg	agccccatct	cgatatttcc											2351
aatcctggct	actttttcta	gagaaaataa	gtcctttttt	tctggccttg	ctaattggcaa											2411
cagaagaaag	ggcttctttg	cgtggtcccc	tgctggtggg	ggtgggtccc	cagggggccc											2471
cctgcggcct	gggccccctt	gcccacggcc	agcttcctgc	tgatgaacat	gctgtttgta											2531
ttgttttagg	aaaccaggct	gttttgtgaa	taaaacgaat	gcatgtttgt	gtcacgaaaa											2591
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	a												2632

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 <212> PRT  
 <213> homo sapiens

<400> 8

Met	Met	Gly	Gly	Glu	Ser	Ala	Asp	Lys	Ala	Thr	Ala	Ala	Ala	Ala	Ala	
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122257 sequence listing May 10 2006.ST25.txt

Ala Ser Leu Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val  
20 25 30

Asp Lys Ser Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser  
35 40 45

Leu Leu Ser Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln  
50 55 60

Leu Thr Leu Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val  
65 70 75 80

Val Gln Glu His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro  
85 90 95

Asp Met Glu Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp  
100 105 110

Phe Pro Tyr Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met  
115 120 125

Thr Pro Ala Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly  
130 135 140

Leu Ala Glu Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser  
145 150 155 160

Gly Lys Lys Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg  
165 170 175

Arg Ile Asn Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly  
180 185 190

His Gln Ile Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro  
195 200 205

Ser Ala Ala Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg  
210 215 220

Trp Phe Gln  
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<210> 9  
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<220>  
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<222> (58)..(1131)

<400> 9



122257 sequence listing May 10 2006.ST25.txt

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gga gcc tct caa gtt gaa gat atg ggg aat ata att tta gca atg att Gly Ala Ser Gln Val Glu Asp Met Gly Asn Ile Ile Leu Ala Met Ile 20 25 30	153
tca gag cct tat aat cac agg ttt tca gat cca gag aga gtg aat tac Ser Glu Pro Tyr Asn His Arg Phe Ser Asp Pro Glu Arg Val Asn Tyr 35 40 45	201
aag ttt gaa agt gga act tgc agc aag atg gaa ctt att gat gat aac Lys Phe Glu Ser Gly Thr Cys Ser Lys Met Glu Leu Ile Asp Asp Asn 50 55 60	249
acc gta gtc agg gca cga ggt tta cca tgg cag tct tca gat caa gat Thr Val Val Arg Ala Arg Gly Leu Pro Trp Gln Ser Ser Asp Gln Asp 65 70 75 80	297
att gca aga ttc ttc aaa gga ctc aat att gcc aag gga ggt gca gca Ile Ala Arg Phe Phe Lys Gly Leu Asn Ile Ala Lys Gly Gly Ala Ala 85 90 95	345
ctt tgt ctg aat gct cag ggt cga agg aac gga gaa gct ctg gtt agg Leu Cys Leu Asn Ala Gln Gly Arg Arg Asn Gly Glu Ala Leu Val Arg 100 105 110	393
ttt gta agt gag gag cac cga gac cta gca cta cag agg cac aaa cat Phe Val Ser Glu Glu His Arg Asp Leu Ala Leu Gln Arg His Lys His 115 120 125	441
cac atg ggg acc cgg tat att gag gtt tac aaa gca aca ggt gaa gat His Met Gly Thr Arg Tyr Ile Glu Val Tyr Lys Ala Thr Gly Glu Asp 130 135 140	489
ttc ctt aaa att gct ggt ggt act tcc aat gag gta gcc cag ttt ctc Phe Leu Lys Ile Ala Gly Gly Thr Ser Asn Glu Val Ala Gln Phe Leu 145 150 155 160	537
tcc aag gaa aat caa gtc att gtt cgc atg cgg ggg ctc cct ttc acg Ser Lys Glu Asn Gln Val Ile Val Arg Met Arg Gly Leu Pro Phe Thr 165 170 175	585
gcc aca gct gaa gaa gtg gtg gcc ttc ttt gga cag cat tgc cct att Ala Thr Ala Glu Glu Val Val Ala Phe Phe Gly Gln His Cys Pro Ile 180 185 190	633
act ggg gga aag gaa ggc atc ctc ttt gtc acc tac cca gat ggt agg Thr Gly Gly Lys Glu Gly Ile Leu Phe Val Thr Tyr Pro Asp Gly Arg 195 200 205	681
cca aca ggg gac gct ttt gtc ctc ttt gcc tgt gag gaa tat gca cag Pro Thr Gly Asp Ala Phe Val Leu Phe Ala Cys Glu Glu Tyr Ala Gln 210 215 220	729
aat gcg ttg agg aag cat aaa gac ttg ttg ggt aaa aga tac att gaa Asn Ala Leu Arg Lys His Lys Asp Leu Leu Gly Lys Arg Tyr Ile Glu 225 230 235 240	777
ctc ttc agg agc aca gca gct gaa gtt cag cag gtg ctg aat cga ttc Leu Phe Arg Ser Thr Ala Ala Glu Val Gln Gln Val Leu Asn Arg Phe 245 250 255	825
tcc tcg gcc cct ctc att cca ctt cca acc cct ccc att att cca gta Ser Ser Ala Pro Leu Ile Pro Leu Pro Thr Pro Pro Ile Ile Pro Val 260 265 270 275 280 285 290	873

122257 sequence listing May 10 2006.ST25.txt

cta cct cag	caa ttt gtg	ccc cct aca	aat gtt aga	gac tgt ata	cgc	921
Leu Pro Gln	Gln Phe Val	Pro Pro Thr	Asn Val Arg	Asp Cys Ile	Arg	
	275	280		285		
ctt cga ggt	ctt ccc tat	gca gcc aca	att gag gac	atc ctg gat	ttc	969
Leu Arg Gly	Leu Pro Tyr	Ala Ala Thr	Ile Glu Asp	Ile Leu Asp	Phe	
	290	295	300			
ctg ggg gag	ttc gcc aca	gat att cgt	act cat ggg	gtt cac atg	gtt	1017
Leu Gly Glu	Phe Ala Thr	Asp Ile Arg	Thr His Gly	Val His Met	Val	
	305	310	315		320	
ttg aat cac	cag ggc cgc	cca tca gga	gat gcc ttt	atc cag atg	aag	1065
Leu Asn His	Gln Gly Arg	Pro Ser Gly	Asp Ala Phe	Ile Gln Met	Lys	
	325		330	335		
tct gcg gac	aga gca ttt	atg gct gca	cag aag tgt	cat aaa aaa	aaa	1113
Ser Ala Asp	Arg Ala Phe	Met Ala Ala	Gln Lys Cys	His Lys Lys	Lys	
	340	345		350		
cat gaa gga	cag ata tgt	tgaagtcttt	cagtgttcag	ctgaggagat		1161
His Glu Gly	Gln Ile Cys					
	355					
gaactttgtg	ttaatggggg	gcactttaaa	tcgaaatggc	ttatccccac	cgccatgtaa	1221
gttaccatgc	ctgtctcctc	cctcctacac	atttccagct	cctgctgcag	ttattcctac	1281
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ccagacacaa	gaaaacttct	agcaaattca	ggggaagttt	gtctacactc	aggctgcagt	1641
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agtttgagct	agtgaagcca	aatcgtaact	tacagcaagc	agcatgcagc	atacctggct	1761
ctttgtgat	tgcaaatagg	catttaaaat	gtgaatttgg	aatcagatgt	ctccattact	1821
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cagtgtctac	catctccacc	atgaactctg	ttaaggaagc	ttcatttttg	tatattcccg	1941
ctcttttctc	ttcatttccc	tgtcttctgc	ataatcatgc	cttcttgcta	agtaattcaa	2001
gcataagatc	ttggaataat	aaaatcacia	tcttaggaga	aagaataaaa	ttgttatattt	2061
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<210> 10  
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 <212> PRT  
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122257 sequence listing May 10 2006.ST25.txt

Met Thr Glu Tyr Leu Asn Phe Glu Lys Ser Ser Ser Val Ser Arg Tyr  
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Gly Ala Ser Gln Val Glu Asp Met Gly Asn Ile Ile Leu Ala Met Ile  
20 25 30

Ser Glu Pro Tyr Asn His Arg Phe Ser Asp Pro Glu Arg Val Asn Tyr  
35 40 45

Lys Phe Glu Ser Gly Thr Cys Ser Lys Met Glu Leu Ile Asp Asp Asn  
50 55 60

Thr Val Val Arg Ala Arg Gly Leu Pro Trp Gln Ser Ser Asp Gln Asp  
65 70 75 80

Ile Ala Arg Phe Phe Lys Gly Leu Asn Ile Ala Lys Gly Gly Ala Ala  
85 90 95

Leu Cys Leu Asn Ala Gln Gly Arg Arg Asn Gly Glu Ala Leu Val Arg  
100 105 110

Phe Val Ser Glu Glu His Arg Asp Leu Ala Leu Gln Arg His Lys His  
115 120 125

His Met Gly Thr Arg Tyr Ile Glu Val Tyr Lys Ala Thr Gly Glu Asp  
130 135 140

Phe Leu Lys Ile Ala Gly Gly Thr Ser Asn Glu Val Ala Gln Phe Leu  
145 150 155 160

Ser Lys Glu Asn Gln Val Ile Val Arg Met Arg Gly Leu Pro Phe Thr  
165 170 175

Ala Thr Ala Glu Glu Val Val Ala Phe Phe Gly Gln His Cys Pro Ile  
180 185 190

Thr Gly Gly Lys Glu Gly Ile Leu Phe Val Thr Tyr Pro Asp Gly Arg  
195 200 205

Pro Thr Gly Asp Ala Phe Val Leu Phe Ala Cys Glu Glu Tyr Ala Gln  
210 215 220

Asn Ala Leu Arg Lys His Lys Asp Leu Leu Gly Lys Arg Tyr Ile Glu  
225 230 235 240

Leu Phe Arg Ser Thr Ala Ala Glu Val Gln Gln Val Leu Asn Arg Phe  
245 250 255

Ser Ser Ala Pro Leu Ile Pro Leu Pro Thr Pro Pro Ile Ile Pro Val  
260 265 270

122257 sequence listing May 10 2006.ST25.txt

Leu Pro Gln Gln Phe Val Pro Pro Thr Asn Val Arg Asp Cys Ile Arg  
275 280 285

Leu Arg Gly Leu Pro Tyr Ala Ala Thr Ile Glu Asp Ile Leu Asp Phe  
290 295 300

Leu Gly Glu Phe Ala Thr Asp Ile Arg Thr His Gly Val His Met Val  
305 310 315 320

Leu Asn His Gln Gly Arg Pro Ser Gly Asp Ala Phe Ile Gln Met Lys  
325 330 335

Ser Ala Asp Arg Ala Phe Met Ala Ala Gln Lys Cys His Lys Lys Lys  
340 345 350

His Glu Gly Gln Ile Cys  
355

<210> 11  
<211> 2808  
<212> DNA  
<213> homo sapiens

<220>  
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<222> (80)..(607)

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cagcagcggc agcggcagc atg tcg gcc ggc gga gcg tca gtc ccg ccg ccc 112  
Met Ser Ala Gly Gly Ala Ser Val Pro Pro Pro  
1 5 10  
ccg aac ccc gcc gtg tcc ttc ccg ccg ccc cgg gtc acc ctg ccc gcc 160  
Pro Asn Pro Ala Val Ser Phe Pro Pro Pro Arg Val Thr Leu Pro Ala  
15 20 25  
ggc ccc gac atc ctg cgg acc tac tcg ggc gcc ttc gtc tgc ctg gag 208  
Gly Pro Asp Ile Leu Arg Thr Tyr Ser Gly Ala Phe Val Cys Leu Glu  
30 35 40  
att ctg ttc ggg ggt ctt gtc tgg att ttg gtt gcc tcc tcc aat gtt 256  
Ile Leu Phe Gly Gly Leu Val Trp Ile Leu Val Ala Ser Ser Asn Val  
45 50 55  
cct cta cct cta cta caa gga tgg gtc atg ttt gtg tcc gtg aca gcg 304  
Pro Leu Pro Leu Leu Gln Gly Trp Val Met Phe Val Ser Val Thr Ala  
60 65 70 75  
ttt ttc ttt tcg ctc ctc ttt ctg ggc atg ttc ctc tct ggc atg gtg 352  
Phe Phe Phe Ser Leu Leu Phe Leu Gly Met Phe Leu Ser Gly Met Val  
80 85 90  
gct caa att gat gct aac tgg aac ttc ctg gat ttt gcc tac cat ttt 400  
Ala Gln Ile Asp Ala Asn Trp Asn Phe Leu Asp Phe Ala Tyr His Phe  
95 100 105  
aca gta ttt gtc ttc tat ttt gga gcc ttt tta ttg gaa gca gca gcc 448  
Thr Val Phe Val Phe Tyr Phe Gly Ala Phe Leu Leu Glu Ala Ala Ala  
110 115 120

## 122257 sequence listing May 10 2006.ST25.txt

aca tcc ctg cat gat ttg cat tgc aat aca acc ata acc ggg cag cca Thr Ser Leu His Asp Leu His Cys Asn Thr Thr Ile Thr Gly Gln Pro 125 130 135	496
ctc ctg agt gat aac cag tat aac ata aac gta gca gcc tca att ttt Leu Leu Ser Asp Asn Gln Tyr Asn Ile Asn Val Ala Ala Ser Ile Phe 140 145 150 155	544
gcc ttt atg acg aca gct tgt tat ggt tgc agt ttg ggt ctg gct tta Ala Phe Met Thr Thr Ala Cys Tyr Gly Cys Ser Leu Gly Leu Ala Leu 160 165 170	592
cga aga tgg cga ccg taacactcct tagaaactgg cagtcgtatg ttagtttcac Arg Arg Trp Arg Pro 175	647
ttgtctactt tatatgtctg atcaatttgg ataccatttt gtccagatgc aaaaacattc	707
caaaagtaat gtgttttagta gagagagact ctaagctcaa gttctggttt atttcattgga	767
tggaatgtta attttattat gatattaaag aaatggcctt ttattttaca tctctcccct	827
ttttcccttt ccccttttat tttcctcctt ttcttttctga aagtttcctt ttatgtccat	887
aaaatacaaa tatattgttc ataaaaaatt agtatccctt ttgtttgggt gctgagtcac	947
ctgaacctta attttaattg gtaattacag cccctaaaaa aaacacattt caaataggct	1007
tcccactaaa ctctatatatt tagtgtaaac caggaattgg cacacttttt ttagaatggg	1067
ccagatggta aatatttatg cttcacggtc catacagtct ctgtcacaac tattcagttc	1127
tgctagtata gcgtgaaagc agctatacac aatacagaaa tgaatgagtg tggttatggt	1187
ctaataaaac ttattttataa aaacaagggg aggctggggt tagcctgtgg gccatagttt	1247
gtcaaccact ggtgtaaaac cttagttata tatgatctgc attttcttga actgatcatt	1307
gaaaacttat aaacctaaca gaaaagccac ataatattta gtgtcattat gcaataatca	1367
cattgccttt gtgttaatag tcaaatactt acctttggag aatacttacc tttggaggaa	1427
tgtataaaat ttctcaggca gagtcctgga tataggaaaa agtaatttat gaagtaaact	1487
tcagttgctt aatcaaaacta atgatagtct aacaactgag caagatcctc atctgagagt	1547
gcttaaaatg ggatccccag agaccattaa ccaatactgg aactggatc tagctactga	1607
tgtcttactt tgagtttatt tatgcttcag aatacagttg tttgccctgt gcatgaatat	1667
acccatattt gtgtgtggat atgtgaagct tttccaaata gagctctcag aagaattaag	1727
tttttacttc taattatttt gcattacttt gagttaaatt tgaatagagt attaaatata	1787
aagttgtaga ttcttatgtg tttttgtatt agcccagaca tctgtaatgt ttttgactg	1847
gtgacagaca aaatctgttt taaaatcata tccagcacia aaactatttc tggctgaata	1907
gcacagaaaa gtattttaac ctacctgtag agatcctcgt catggaaagg tgccaaactg	1967
ttttgaatgg aaggacaagt aagagtgagg ccacagttcc caccacacga gggcttttgt	2027
attgttctac tttttcagcc ctttactttc tggctgaagc atccccttg agtgccatgt	2087
ataagttggg ctattagagt tcatggaaca tagaacaacc atgaatgagt ggcatgatcc	2147
gtgcttaatg atcaagtgtt acttatctaa taatcctcta gaaagaaccc tgttagatct	2207

122257 sequence listing May 10 2006.ST25.txt

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tggtttgtga taaaaatata aagacagaag acatgaggaa aaacaaaagg tttgaggaaa 2267
tcaggcatat gactttatac ttaacatcag atcttttcta taatataccta ctacttttgg 2327
tttcctagct ccataaccaca cacctaaacc tgtattatga attacatatt acaaagtcatt 2387
aaatgtgcca tatggatata cagtacattc tagttggaat cgtttactct gctagaattt 2447
aggtgtgaga ttttttgttt cccaggtata gcaggcttat gtttggtggc attaaattgg 2507
tttctttaa atgcttttgg ggcacttttg taaacagatt gcttctagat tgttacaaac 2567
caagcctaag acacatctgt gaatacttag atttgtagct taatcacatt ctagacttgt 2627
gagttgaatg acaaagcagt tgaacaaaaa ttatggcatt taagaattta acatgtctta 2687
gctgtaaaaa tgagaaaagt ttggttggtt ttaaaatctg gtaactccat gatgaaaaga 2747
aatattttt atacgtgtta tgtctctaataaagtattca tttgataaaa aaaaaaaaaa 2807
a 2808

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<210> 12
<211> 176
<212> PRT
<213> homo sapiens

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1 5 10 15

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Ser Phe Pro Pro Pro Arg Val Thr Leu Pro Ala Gly Pro Asp Ile Leu
20 25 30

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Arg Thr Tyr Ser Gly Ala Phe Val Cys Leu Glu Ile Leu Phe Gly Gly
35 40 45

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Leu Val Trp Ile Leu Val Ala Ser Ser Asn Val Pro Leu Pro Leu Leu
50 55 60

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Gln Gly Trp Val Met Phe Val Ser Val Thr Ala Phe Phe Phe Ser Leu
65 70 75 80

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Leu Phe Leu Gly Met Phe Leu Ser Gly Met Val Ala Gln Ile Asp Ala
85 90 95

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Asn Trp Asn Phe Leu Asp Phe Ala Tyr His Phe Thr Val Phe Val Phe
100 105 110

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Tyr Phe Gly Ala Phe Leu Leu Glu Ala Ala Ala Thr Ser Leu His Asp
115 120 125

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Leu His Cys Asn Thr Thr Ile Thr Gly Gln Pro Leu Leu Ser Asp Asn
130 135 140

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Gln Tyr Asn Ile Asn Val Ala Ala Ser Ile Phe Ala Phe Met Thr Thr

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## 122257 sequence listing May 10 2006.ST25.txt

145 150 155 160

Ala Cys Tyr Gly Cys Ser Leu Gly Leu Ala Leu Arg Arg Trp Arg Pro  
165 170 175

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<213> homo sapiens

<220>  
<221> CDS  
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gggaag atg ccc cgg ccg gag ctg ccc ctg ccg gag ggc tgg gag gag 108  
Met Pro Arg Pro Glu Leu Pro Leu Pro Glu Gly Trp Glu Glu  
1 5 10  
gcg cgc gac ttc gac ggc aag gtc tac tac ata gac cac acg aac cgc 156  
Ala Arg Asp Phe Asp Gly Lys Val Tyr Tyr Ile Asp His Thr Asn Arg  
15 20 25 30  
acc acc agc tgg atc gac ccg cgg gac agg tac acc aaa ccg ctc acc 204  
Thr Thr Ser Trp Ile Asp Pro Arg Asp Arg Tyr Thr Lys Pro Leu Thr  
35 40 45  
ttt gct gac tgc att agt gat gag ttg ccg cta gga tgg gaa gag gca 252  
Phe Ala Asp Cys Ile Ser Asp Glu Leu Pro Leu Gly Trp Glu Glu Ala  
50 55 60  
tat gac cca cag gtt gga gat tac ttc ata gac cac aac acc aaa acc 300  
Tyr Asp Pro Gln Val Gly Asp Tyr Phe Ile Asp His Asn Thr Lys Thr  
65 70 75  
act cag att gag gat cct cga gta caa tgg cgg cgg gag cag gaa cat 348  
Thr Gln Ile Glu Asp Pro Arg Val Gln Trp Arg Arg Glu Gln Glu His  
80 85 90  
atg ctg aag gat tac ctg gtg gtg gcc cag gag gct ctg agt gca caa 396  
Met Leu Lys Asp Tyr Leu Val Val Ala Gln Glu Ala Leu Ser Ala Gln  
95 100 105 110  
aag gag atc tac cag gtg aag cag cag cgc ctg gag ctt gca cag cag 444  
Lys Glu Ile Tyr Gln Val Lys Gln Gln Arg Leu Glu Leu Ala Gln Gln  
115 120 125  
gag tac cag caa ctg cat gcc gtc tgg gag cat aag ctg ggc tcc cag 492  
Glu Tyr Gln Gln Leu His Ala Val Trp Glu His Lys Leu Gly Ser Gln  
130 135 140  
gtc agc ttg gtc tct ggt tca tca tcc agc tcc aag tat gac cct gag 540  
Val Ser Leu Val Ser Gly Ser Ser Ser Ser Ser Lys Tyr Asp Pro Glu  
145 150 155  
atc ctg aaa gct gaa att gcc act gca aaa tcc cgg gtc aac aag ctg 588  
Ile Leu Lys Ala Glu Ile Ala Thr Ala Lys Ser Arg Val Asn Lys Leu  
160 165 170  
aag aga gag atg gtt cac ctc cag cac gag ctg cag ttc aaa gag cgt 636  
Lys Arg Glu Met Val His Leu Gln His Glu Leu Gln Phe Lys Glu Arg  
175 180 185 190

122257 sequence listing May 10 2006.ST25.txt

ggc ttt cag acc ctg aag aaa atc gat aag aaa atg tct gat gct cag Gly Phe Gln Thr Leu Lys Lys Ile Asp Lys Lys Met Ser Asp Ala Gln 195 200 205	684
ggc agc tac aaa ctg gat gaa gct cag gct gtc ttg aga gaa aca aaa Gly Ser Tyr Lys Leu Asp Glu Ala Gln Val Leu Arg Glu Thr Lys 210 215 220	732
gcc atc aaa aag gct att acc tgt ggg gaa aag gaa aag caa gat ctc Ala Ile Lys Lys Ala Ile Thr Cys Gly Glu Lys Glu Lys Gln Asp Leu 225 230 235	780
att aag agc ctt gcc atg ttg aag gac ggc ttc cgc act gac agg ggg Ile Lys Ser Leu Ala Met Leu Lys Asp Gly Phe Arg Thr Asp Arg Gly 240 245 250	828
tct cac tca gac ctg tgg tcc agc agc agc tct ctg gag agt tcg agt Ser His Ser Asp Leu Trp Ser Ser Ser Ser Leu Glu Ser Ser Ser 255 260 265 270	876
ttc ccg cta ccg aaa cag tac ctg gat gtg agc tcc cag aca gac atc Phe Pro Leu Pro Lys Gln Tyr Leu Asp Val Ser Ser Gln Thr Asp Ile 275 280 285	924
tcg gga agc ttc ggc atc aac agc aac aat cag ttg gca gag aag gtc Ser Gly Ser Phe Gly Ile Asn Ser Asn Asn Gln Leu Ala Glu Lys Val 290 295 300	972
aga ttg cgc ctt cga tat gaa gag gct aag aga agg atc gcc aac ctg Arg Leu Arg Leu Arg Tyr Glu Glu Ala Lys Arg Arg Ile Ala Asn Leu 305 310 315	1020
aag atc cag ctg gcc aag ctt gac agt gag gcc tgg cct ggg gtg ctg Lys Ile Gln Leu Ala Lys Leu Asp Ser Glu Ala Trp Pro Gly Val Leu 320 325 330	1068
gac tca gag agg gac cgg ctg atc ctt atc aac gag aag gag gag ctg Asp Ser Glu Arg Asp Arg Leu Ile Leu Ile Asn Glu Lys Glu Glu Leu 335 340 345 350	1116
ctg aag gag atg cgc ttc atc agc ccc cgc aag tgg acc cag ggg gag Leu Lys Glu Met Arg Phe Ile Ser Pro Arg Lys Trp Thr Gln Gly Glu 355 360 365	1164
gtg gag cag ctg gag atg gcc cgg aag cgg ctg gaa aag gac ctg cag Val Glu Gln Leu Glu Met Ala Arg Lys Arg Leu Glu Lys Asp Leu Gln 370 375 380	1212
gca gcc cgg gac acc cag agc aag gcg ctg acg gag agg tta aag tta Ala Ala Arg Asp Thr Gln Ser Lys Ala Leu Thr Glu Arg Leu Lys Leu 385 390 395	1260
aac agt aag agg aac cag ctt gtg aga gaa ctg gag gaa gcc acc cgg Asn Ser Lys Arg Asn Gln Leu Val Arg Glu Leu Glu Glu Ala Thr Arg 400 405 410	1308
cag gtg gca act ctg cac tcc cag ctg aaa agt ctc tca agc agc atg Gln Val Ala Thr Leu His Ser Gln Leu Lys Ser Leu Ser Ser Ser Met 415 420 425 430	1356
cag tcc ctg tcc tca ggc agc agc ccc gga tcc ctc acg tcc agc cgg Gln Ser Leu Ser Ser Gly Ser Ser Pro Gly Ser Leu Thr Ser Ser Arg 435 440 445	1404
ggc tcc ctg gtt gca tcc agc ctg gac tcc tcc act tca gcc agc ttc Gly Ser Leu Val Ala Ser Ser Leu Asp Ser Ser Thr Ser Ala Ser Phe 450 455 460	1452



## 122257 sequence listing May 10 2006.ST25.txt

act gac ctc tac tat gac ccc ttt gag cag ctg gac tca gag ctg cag Thr Asp Leu Tyr Tyr Asp Pro Phe Glu Gln Leu Asp Ser Glu Leu Gln 465 470 475	1500
agc aag gtg gag ttc ctg ctc ctg gag ggg gcc acc ggc ttc cgg ccc Ser Lys Val Glu Phe Leu Leu Leu Glu Gly Ala Thr Gly Phe Arg Pro 480 485 490	1548
tca ggc tgc atc acc acc atc cac gag gat gag gtg gcc aag acc cag Ser Gly Cys Ile Thr Thr Ile His Glu Asp Glu Val Ala Lys Thr Gln 495 500 505 510	1596
aag gca gag gga ggt ggc cgc ctg cag gct ctg cgt tcc ctg tct ggc Lys Ala Glu Gly Gly Arg Leu Gln Ala Leu Arg Ser Leu Ser Gly 515 520 525	1644
acc cca aag tcc atg acc tcc cta tcc cca cgt tcc tct ctc tcc tcc Thr Pro Lys Ser Met Thr Ser Leu Ser Pro Arg Ser Ser Leu Ser Ser 530 535 540	1692
ccc tcc cca ccc tgt tcc cct ctc atg gct gac ccc ctc ctg gct ggt Pro Ser Pro Pro Cys Ser Pro Leu Met Ala Asp Pro Leu Ala Gly 545 550 555	1740
gat gcc ttc ctc aac tcc ttg gag ttt gaa gac ccg gag ctg agt gcc Asp Ala Phe Leu Asn Ser Leu Glu Phe Glu Asp Pro Glu Leu Ser Ala 560 565 570	1788
act ctt tgt gaa ctg agc ctt ggt aac agc gcc cag gaa aga tac cgg Thr Leu Cys Glu Leu Ser Leu Gly Asn Ser Ala Gln Glu Arg Tyr Arg 575 580 585 590	1836
ctg gag gaa cca gga acg gag ggc aag cag ctg ggc caa gct gtg aat Leu Glu Glu Pro Gly Thr Glu Gly Lys Gln Leu Gly Gln Ala Val Asn 595 600 605	1884
acg gcc cag ggg tgt ggc ctg aaa gtg gcc tgt gtc tca gcc gcc gta Thr Ala Gln Gly Cys Gly Leu Lys Val Ala Cys Val Ser Ala Ala Val 610 615 620	1932
tcg gac gag tca gtg gct gga gac agt ggt gtg tac gag gct tcc gtg Ser Asp Glu Ser Val Ala Gly Asp Ser Gly Val Tyr Glu Ala Ser Val 625 630 635	1980
cag aga ctg ggt gct tca gaa gct gct gca ttt gac agt gac gaa tcg Gln Arg Leu Gly Ala Ser Glu Ala Ala Phe Asp Ser Asp Glu Ser 640 645 650	2028
gaa gca gtg ggt gcg acc cga att cag att gcc ctg aag tat gat gag Glu Ala Val Gly Ala Thr Arg Ile Gln Ile Ala Leu Lys Tyr Asp Glu 655 660 665 670	2076
aag aat aag caa ttt gca ata tta atc atc cag ctg agt aac ctt tct Lys Asn Lys Gln Phe Ala Ile Leu Ile Ile Gln Leu Ser Asn Leu Ser 675 680 685	2124
gct ctg ttg cag caa caa gac cag aaa gtg aat atc cgc gtg gct gtc Ala Leu Leu Gln Gln Gln Asp Gln Lys Val Asn Ile Arg Val Ala Val 690 695 700	2172
ctt cct tgc tct gaa agc aca acc tgc ctg ttc cgg acc cgg cct ctg Leu Pro Cys Ser Glu Ser Thr Thr Cys Leu Phe Arg Thr Arg Pro Leu 705 710 715	2220
gac gcc tca gac act cta gtg ttc aat gag gtg ttc tgg gta tcc atg Asp Ala Ser Asp Thr Leu Val Phe Asn Glu Val Phe Trp Val Ser Met 720 725 730	2268

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tcc	tat	cca	gcc	ctt	cac	cag	aag	acc	tta	aga	gtc	gat	gtc	tgt	acc	2316
Ser	Tyr	Pro	Ala	Leu	His	Gln	Lys	Thr	Leu	Arg	Val	Asp	Val	Cys	Thr	
735					740					745					750	
acc	gac	agg	agc	cat	ctg	gaa	gag	tgc	ctg	gga	ggc	gcc	cag	atc	agc	2364
Thr	Asp	Arg	Ser	His	Leu	Glu	Glu	Cys	Leu	Gly	Gly	Ala	Gln	Ile	Ser	
				755					760					765		
ctg	gcg	gag	gtc	tgc	cgg	tct	ggg	gag	agg	tcg	act	cgc	tgg	tac	aac	2412
Leu	Ala	Glu	Val	Cys	Arg	Ser	Gly	Glu	Arg	Ser	Thr	Arg	Trp	Tyr	Asn	
			770				775						780			
ctt	ctc	agc	tac	aaa	tac	ttg	aag	aag	cag	agc	agg	gag	ctc	aag	cca	2460
Leu	Leu	Ser	Tyr	Lys	Tyr	Leu	Lys	Lys	Gln	Ser	Arg	Glu	Leu	Lys	Pro	
		785					790					795				
gtg	gga	gtt	atg	gcc	cct	gcc	tca	ggg	cct	gcc	agc	acg	gac	gct	gtg	2508
Val	Gly	Val	Met	Ala	Pro	Ala	Ser	Gly	Pro	Ala	Ser	Thr	Asp	Ala	Val	
	800					805					810					
tct	gct	ctg	ttg	gaa	cag	aca	gca	gtg	gag	ctg	gag	aag	agg	cag	gag	2556
Ser	Ala	Leu	Leu	Glu	Gln	Thr	Ala	Val	Glu	Leu	Glu	Lys	Arg	Gln	Glu	
815					820					825					830	
ggc	agg	agc	agc	aca	cag	aca	ctg	gaa	gac	agc	tgg	agg	tat	gag	gag	2604
Gly	Arg	Ser	Ser	Thr	Gln	Thr	Leu	Glu	Asp	Ser	Trp	Arg	Tyr	Glu	Glu	
				835					840					845		
acc	agt	gag	aat	gag	gca	gta	gcc	gag	gaa	gag	gag	gag	gag	gtg	gag	2652
Thr	Ser	Glu	Asn	Glu	Ala	Val	Ala	Glu	Glu	Glu	Glu	Glu	Glu	Val	Glu	
			850					855					860			
gag	gag	gag	gga	gaa	gag	gat	gtt	ttc	acc	gag	aaa	gcc	tca	cct	gat	2700
Glu	Glu	Glu	Gly	Glu	Glu	Asp	Val	Phe	Thr	Glu	Lys	Ala	Ser	Pro	Asp	
		865					870					875				
atg	gat	ggg	tac	cca	gca	tta	aag	gtg	gac	aaa	gag	acc	aac	acg	gag	2748
Met	Asp	Gly	Tyr	Pro	Ala	Leu	Lys	Val	Asp	Lys	Glu	Thr	Asn	Thr	Glu	
	880					885					890					
acc	ccg	gcc	cca	tcc	ccc	aca	gtg	gtg	cga	cct	aag	gac	cgg	aga	gtg	2796
Thr	Pro	Ala	Pro	Ser	Pro	Thr	Val	Val	Arg	Pro	Lys	Asp	Arg	Arg	Val	
895					900					905					910	
ggc	acc	ccg	tcc	cag	ggg	cca	ttt	ctt	cga	ggg	agc	acc	atc	atc	cgc	2844
Gly	Thr	Pro	Ser	Gln	Gly	Pro	Phe	Leu	Arg	Gly	Ser	Thr	Ile	Ile	Arg	
				915					920					925		
tct	aag	acc	ttc	tcc	cca	gga	ccc	cag	agc	cag	tac	gtg	tgc	cgg	ctg	2892
Ser	Lys	Thr	Phe	Ser	Pro	Gly	Pro	Gln	Ser	Gln	Tyr	Val	Cys	Arg	Leu	
			930					935					940			
aat	cgg	agt	gat	agt	gac	agc	tcc	act	ctg	tcc	aaa	aag	cca	cct	ttt	2940
Asn	Arg	Ser	Asp	Ser	Asp	Ser	Ser	Thr	Leu	Ser	Lys	Lys	Pro	Pro	Phe	
		945					950					955				
gtt	cga	aac	tcc	ctg	gag	cga	cgc	agc	gtc	cgg	atg	aag	cgg	cct	tcc	2988
Val	Arg	Asn	Ser	Leu	Glu	Arg	Arg	Ser	Val	Arg	Met	Lys	Arg	Pro	Ser	
	960					965					970					
tcg	gtc	aag	tcg	ctg	cgc	tcc	gag	cgt	ctg	atc	cgt	acc	tcg	ctg	gac	3036
Ser	Val	Lys	Ser	Leu	Arg	Ser	Glu	Arg	Leu	Ile	Arg	Thr	Ser	Leu	Asp	
975					980					985					990	
ctg	gag	tta	gac	ctg	cag	gcg	aca	aga	acc	tgg	cac	agc	caa	ctg	acc	3084
Leu	Glu	Leu	Asp	Leu	Gln	Ala	Thr	Arg	Thr	Trp	His	Ser	Gln	Leu	Thr	
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cag gag atc tcg gtg ctg aag gag ctc aag gag cag ctg gaa caa	3129
Gln Glu Ile Ser Val Leu Lys Glu Leu Lys Glu Gln Leu Glu Gln	
1010 1015 1020	
gcc aag agc cac ggg gag aag gag ctg cca cag tgg ttg cgt gag	3174
Ala Lys Ser His Gly Glu Lys Glu Leu Pro Gln Trp Leu Arg Glu	
1025 1030 1035	
gac gag cgt ttc cgc ctg ctg ctg agg atg ctg gag aag cgg cag	3219
Asp Glu Arg Phe Arg Leu Leu Leu Arg Met Leu Glu Lys Arg Gln	
1040 1045 1050	
atg gac cga gcg gag cac aag ggt gag ctt cag aca gac aag atg	3264
Met Asp Arg Ala Ala Glu His Lys Gly Glu Leu Gln Thr Asp Lys Met	
1055 1060 1065	
atg agg gca gct gcc aag gat gtg cac agg ctg cga ggc cag agc	3309
Met Arg Ala Ala Ala Lys Asp Val His Arg Leu Arg Gly Gln Ser	
1070 1075 1080	
tgt aag gaa ccc cca gaa gtt cag tct ttc agg gag aag atg gca	3354
Cys Lys Glu Pro Pro Glu Val Gln Ser Phe Arg Glu Lys Met Ala	
1085 1090 1095	
ttt ttc acc cgg cct cgg atg aat atc cca gct ctg tct gca gat	3399
Phe Phe Thr Arg Pro Arg Met Asn Ile Pro Ala Leu Ser Ala Asp	
1100 1105 1110	
gac gtc taatcgccag aaaagtattt cctttgttcc actgaccagg ctgtgaacat	3455
Asp Val	
tgactgtggc taaagttatt tatgtggtgt tatatgaagg tactgagtca caagtcctct	3515
agtgtctcttg ttggtttgaa gatgaaccga ctttttagtt tgggtcctac tgttgttatt	3575
aaaaacagaa caaaaacaaa acacacacac acacaaaaac agaaacaaaa aaaaccagca	3635
ttaaaataat aagattgtat agtttgtata tttaggagtg ttttttggg aaagaaaatt	3695
taaatgaact aaagcagtat tgagttgctg ctcttcttaa aatcgtttag attttttttg	3755
gtttgtacag ctccaccttt tagaggtctt actgcaataa gaagtaatgc ctggggggacg	3815
gtaatcctaa taggacgtcc cgcacttgct acagtacagc taatttttcc tagttaacat	3875
attttgtaca atattaaaaa aatgcacaga aaccattggg ggggattcag aggtgcatcc	3935
acggatcttc ttgagctgtg acgtgttttt atgtggctgc ccaacgtgga gcgggcagtg	3995
tgataggctg ggtgggctaa gcagcctagt ctatgtgggt gacaggccac gctgggtctca	4055
gatgcccagt gaagccacta acatgagtga ggggagggct gtggggaact ccattcagtt	4115
ttatctccat caataaagtg gcctttcaaa aagaaaaaaa aaaaaaaaaa aaaaaa	4171
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Met Pro Arg Pro Glu Leu Pro Leu Pro Glu Gly Trp Glu Glu Ala Arg	
1 5 10 15	

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Asp Phe Asp Gly Lys Val Tyr Tyr Ile Asp His Thr Asn Arg Thr Thr  
20 25 30

Ser Trp Ile Asp Pro Arg Asp Arg Tyr Thr Lys Pro Leu Thr Phe Ala  
35 40 45

Asp Cys Ile Ser Asp Glu Leu Pro Leu Gly Trp Glu Glu Ala Tyr Asp  
50 55 60

Pro Gln Val Gly Asp Tyr Phe Ile Asp His Asn Thr Lys Thr Thr Gln  
65 70 75 80

Ile Glu Asp Pro Arg Val Gln Trp Arg Arg Glu Gln Glu His Met Leu  
85 90 95

Lys Asp Tyr Leu Val Val Ala Gln Glu Ala Leu Ser Ala Gln Lys Glu  
100 105 110

Ile Tyr Gln Val Lys Gln Gln Arg Leu Glu Leu Ala Gln Gln Glu Tyr  
115 120 125

Gln Gln Leu His Ala Val Trp Glu His Lys Leu Gly Ser Gln Val Ser  
130 135 140

Leu Val Ser Gly Ser Ser Ser Ser Ser Lys Tyr Asp Pro Glu Ile Leu  
145 150 155 160

Lys Ala Glu Ile Ala Thr Ala Lys Ser Arg Val Asn Lys Leu Lys Arg  
165 170 175

Glu Met Val His Leu Gln His Glu Leu Gln Phe Lys Glu Arg Gly Phe  
180 185 190

Gln Thr Leu Lys Lys Ile Asp Lys Lys Met Ser Asp Ala Gln Gly Ser  
195 200 205

Tyr Lys Leu Asp Glu Ala Gln Ala Val Leu Arg Glu Thr Lys Ala Ile  
210 215 220

Lys Lys Ala Ile Thr Cys Gly Glu Lys Glu Lys Gln Asp Leu Ile Lys  
225 230 235 240

Ser Leu Ala Met Leu Lys Asp Gly Phe Arg Thr Asp Arg Gly Ser His  
245 250 255

Ser Asp Leu Trp Ser Ser Ser Ser Ser Leu Glu Ser Ser Ser Phe Pro  
260 265 270

Leu Pro Lys Gln Tyr Leu Asp Val Ser Ser Gln Thr Asp Ile Ser Gly  
275 280 285

122257 sequence listing May 10 2006.ST25.txt

Ser Phe Gly Ile Asn Ser Asn Asn Gln Leu Ala Glu Lys Val Arg Leu  
290 295 300

Arg Leu Arg Tyr Glu Glu Ala Lys Arg Arg Ile Ala Asn Leu Lys Ile  
305 310 315 320

Gln Leu Ala Lys Leu Asp Ser Glu Ala Trp Pro Gly Val Leu Asp Ser  
325 330 335

Glu Arg Asp Arg Leu Ile Leu Ile Asn Glu Lys Glu Glu Leu Leu Lys  
340 345 350

Glu Met Arg Phe Ile Ser Pro Arg Lys Trp Thr Gln Gly Glu Val Glu  
355 360 365

Gln Leu Glu Met Ala Arg Lys Arg Leu Glu Lys Asp Leu Gln Ala Ala  
370 375 380

Arg Asp Thr Gln Ser Lys Ala Leu Thr Glu Arg Leu Lys Leu Asn Ser  
385 390 395 400

Lys Arg Asn Gln Leu Val Arg Glu Leu Glu Glu Ala Thr Arg Gln Val  
405 410 415

Ala Thr Leu His Ser Gln Leu Lys Ser Leu Ser Ser Ser Met Gln Ser  
420 425 430

Leu Ser Ser Gly Ser Ser Pro Gly Ser Leu Thr Ser Ser Arg Gly Ser  
435 440 445

Leu Val Ala Ser Ser Leu Asp Ser Ser Thr Ser Ala Ser Phe Thr Asp  
450 455 460

Leu Tyr Tyr Asp Pro Phe Glu Gln Leu Asp Ser Glu Leu Gln Ser Lys  
465 470 475 480

Val Glu Phe Leu Leu Leu Glu Gly Ala Thr Gly Phe Arg Pro Ser Gly  
485 490 495

Cys Ile Thr Thr Ile His Glu Asp Glu Val Ala Lys Thr Gln Lys Ala  
500 505 510

Glu Gly Gly Gly Arg Leu Gln Ala Leu Arg Ser Leu Ser Gly Thr Pro  
515 520 525

Lys Ser Met Thr Ser Leu Ser Pro Arg Ser Ser Leu Ser Ser Pro Ser  
530 535 540

Pro Pro Cys Ser Pro Leu Met Ala Asp Pro Leu Leu Ala Gly Asp Ala  
545 550 555 560

122257 sequence listing May 10 2006.ST25.txt

Phe	Leu	Asn	Ser	Leu	Glu	Phe	Glu	Asp	Pro	Glu	Leu	Ser	Ala	Thr	Leu
				565					570						575
Cys	Glu	Leu	Ser	Leu	Gly	Asn	Ser	Ala	Gln	Glu	Arg	Tyr	Arg	Leu	Glu
			580					585					590		
Glu	Pro	Gly	Thr	Glu	Gly	Lys	Gln	Leu	Gly	Gln	Ala	Val	Asn	Thr	Ala
		595					600					605			
Gln	Gly	Cys	Gly	Leu	Lys	Val	Ala	Cys	Val	Ser	Ala	Ala	Val	Ser	Asp
	610					615					620				
Glu	Ser	Val	Ala	Gly	Asp	Ser	Gly	Val	Tyr	Glu	Ala	Ser	Val	Gln	Arg
625					630					635					640
Leu	Gly	Ala	Ser	Glu	Ala	Ala	Ala	Phe	Asp	Ser	Asp	Glu	Ser	Glu	Ala
				645					650					655	
Val	Gly	Ala	Thr	Arg	Ile	Gln	Ile	Ala	Leu	Lys	Tyr	Asp	Glu	Lys	Asn
			660					665					670		
Lys	Gln	Phe	Ala	Ile	Leu	Ile	Ile	Gln	Leu	Ser	Asn	Leu	Ser	Ala	Leu
		675					680					685			
Leu	Gln	Gln	Gln	Asp	Gln	Lys	Val	Asn	Ile	Arg	Val	Ala	Val	Leu	Pro
	690					695					700				
Cys	Ser	Glu	Ser	Thr	Thr	Cys	Leu	Phe	Arg	Thr	Arg	Pro	Leu	Asp	Ala
705					710					715					720
Ser	Asp	Thr	Leu	Val	Phe	Asn	Glu	Val	Phe	Trp	Val	Ser	Met	Ser	Tyr
				725					730					735	
Pro	Ala	Leu	His	Gln	Lys	Thr	Leu	Arg	Val	Asp	Val	Cys	Thr	Thr	Asp
			740					745					750		
Arg	Ser	His	Leu	Glu	Glu	Cys	Leu	Gly	Gly	Ala	Gln	Ile	Ser	Leu	Ala
		755					760					765			
Glu	Val	Cys	Arg	Ser	Gly	Glu	Arg	Ser	Thr	Arg	Trp	Tyr	Asn	Leu	Leu
	770					775					780				
Ser	Tyr	Lys	Tyr	Leu	Lys	Lys	Gln	Ser	Arg	Glu	Leu	Lys	Pro	Val	Gly
785					790					795					800
Val	Met	Ala	Pro	Ala	Ser	Gly	Pro	Ala	Ser	Thr	Asp	Ala	Val	Ser	Ala
				805					810					815	
Leu	Leu	Glu	Gln	Thr	Ala	Val	Glu	Leu	Glu	Lys	Arg	Gln	Glu	Gly	Arg
			820				825						830		

122257 sequence listing May 10 2006.ST25.txt

Ser Ser Thr Gln Thr Leu Glu Asp Ser Trp Arg Tyr Glu Glu Thr Ser  
835 840 845

Glu Asn Glu Ala Val Ala Glu Glu Glu Glu Glu Glu Val Glu Glu Glu  
850 855 860

Glu Gly Glu Glu Asp Val Phe Thr Glu Lys Ala Ser Pro Asp Met Asp  
865 870 875 880

Gly Tyr Pro Ala Leu Lys Val Asp Lys Glu Thr Asn Thr Glu Thr Pro  
885 890 895

Ala Pro Ser Pro Thr Val Val Arg Pro Lys Asp Arg Arg Val Gly Thr  
900 905 910

Pro Ser Gln Gly Pro Phe Leu Arg Gly Ser Thr Ile Ile Arg Ser Lys  
915 920 925

Thr Phe Ser Pro Gly Pro Gln Ser Gln Tyr Val Cys Arg Leu Asn Arg  
930 935 940

Ser Asp Ser Asp Ser Ser Thr Leu Ser Lys Lys Pro Pro Phe Val Arg  
945 950 955 960

Asn Ser Leu Glu Arg Arg Ser Val Arg Met Lys Arg Pro Ser Ser Val  
965 970 975

Lys Ser Leu Arg Ser Glu Arg Leu Ile Arg Thr Ser Leu Asp Leu Glu  
980 985 990

Leu Asp Leu Gln Ala Thr Arg Thr Trp His Ser Gln Leu Thr Gln Glu  
995 1000 1005

Ile Ser Val Leu Lys Glu Leu Lys Glu Gln Leu Glu Gln Ala Lys  
1010 1015 1020

Ser His Gly Glu Lys Glu Leu Pro Gln Trp Leu Arg Glu Asp Glu  
1025 1030 1035

Arg Phe Arg Leu Leu Leu Arg Met Leu Glu Lys Arg Gln Met Asp  
1040 1045 1050

Arg Ala Glu His Lys Gly Glu Leu Gln Thr Asp Lys Met Met Arg  
1055 1060 1065

Ala Ala Ala Lys Asp Val His Arg Leu Arg Gly Gln Ser Cys Lys  
1070 1075 1080

Glu Pro Pro Glu Val Gln Ser Phe Arg Glu Lys Met Ala Phe Phe  
1085 1090 1095

122257 sequence listing May 10 2006.ST25.txt  
 Thr Arg Pro Arg Met Asn Ile Pro Ala Leu Ser Ala Asp Asp Val  
 1100 1105 1110

<210> 15  
 <211> 1294  
 <212> DNA  
 <213> homo sapiens

<220>  
 <221> CDS  
 <222> (198)..(857)

<400> 15  
 caaagccaca ggcaggtgca ggcgcagccg cggcgagagc gtatggagcc gagccgtag 60  
 cgcgcgccgt cgggtgagtca gtccgtccgt ccgtccgtcc gtcggggcgc cgcagctccc 120  
 gccaggccca gcggcccccgg cccctcgtct ccccgacccc ggagccaccc ggtggagcgg 180  
 gccttgccgc ggcagcc atg tcc atg ggc ctg gag atc acg ggc acc gcg 230  
                   Met Ser Met Gly Leu Glu Ile Thr Gly Thr Ala  
                   1                  5                  10  
 ctg gcc gtg ctg ggc tgg ctg ggc acc atc gtg tgc tgc gcg ttg ccc 278  
 Leu Ala Val Leu Gly Trp Leu Gly Thr Ile Val Cys Cys Ala Leu Pro  
                   15                  20                  25  
 atg tgg cgc gtg tgc gcc ttc atc ggc agc aac atc atc acg tgc cag 326  
 Met Trp Arg Val Ser Ala Phe Ile Gly Ser Asn Ile Ile Thr Ser Gln  
                   30                  35                  40  
 aac atc tgg gag ggc ctg tgg atg aac tgc gtg gtg cag agc acc ggc 374  
 Asn Ile Trp Glu Gly Leu Trp Met Asn Cys Val Val Gln Ser Thr Gly  
                   45                  50                  55  
 cag atg cag tgc aag gtg tac gac tgc ctg ctg gca ctg cca cag gac 422  
 Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp  
 60                  65                  70                  75  
 ctt cag gcg gcc cgc gcc ctc atc gtg gtg gcc atc ctg ctg gcc gcc 470  
 Leu Gln Ala Ala Arg Ala Leu Ile Val Val Ala Ile Leu Leu Ala Ala  
                   80                  85                  90  
 ttc ggg ctg cta gtg gcg ctg gtg ggc gcc cag tgc acc aac tgc gtg 518  
 Phe Gly Leu Leu Val Ala Leu Val Gly Ala Gln Cys Thr Asn Cys Val  
                   95                  100                  105  
 cag gac gac acg gcc aag gcc aag atc acc atc gtg gca ggc gtg ctg 566  
 Gln Asp Asp Thr Ala Lys Ala Lys Ile Thr Ile Val Ala Gly Val Leu  
                   110                  115                  120  
 ttc ctt ctc gcc gcc ctg ctc acc ctc gtg ccg gtg tcc tgg tgc gcc 614  
 Phe Leu Leu Ala Ala Leu Leu Thr Leu Val Pro Val Ser Trp Ser Ala  
                   125                  130                  135  
 aac acc att atc cgg gac ttc tac aac ccc gtg gtg ccc gag gcg cag 662  
 Asn Thr Ile Ile Arg Asp Phe Tyr Asn Pro Val Val Pro Glu Ala Gln  
                   140                  145                  150                  155  
 aag cgc gag atg ggc gcg ggc ctg tac gtg ggc tgg gcg gcc gcg gcg 710  
 Lys Arg Glu Met Gly Ala Gly Leu Tyr Val Gly Trp Ala Ala Ala Ala  
                   160                  165                  170  
 ctg cag ctg ctg ggg ggc gcg ctg ctc tgc tgc tgc tgt ccc cca cgc 758  
 Leu Gln Leu Leu Gly Gly Ala Leu Leu Cys Cys Ser Cys Pro Pro Arg  
                   175                  180                  185



122257 sequence listing May 10 2006.ST25.txt

gag aag aag tac acg gcc acc aag gtc gtc tac tcc gcg ccg cgc tcc Glu Lys Lys Tyr Thr Ala Thr Lys Val Val Tyr Ser Ala Pro Arg Ser 190 195 200	806
acc ggc ccg gga gcc agc ctg ggc aca ggc tac gac cgc aag gac tac Thr Gly Pro Gly Ala Ser Leu Gly Thr Gly Tyr Asp Arg Lys Asp Tyr 205 210 215	854
gtc taagggacag acgcagggag accccaccac caccaccacc accaacacca Val 220	907
ccaccaccac cgcgagctgg agcgcgcacc aggccatcca gcgtgcagcc ttgcctcgga	967
ggccagccca ccccccagaag ccaggaagcc cccgcgctgg actggggcag cttccccagc	1027
agccacggct ttgcgggccc ggcagtcgac ttcggggccc agggaccaac ctgcatggac	1087
tgtgaaacct cacccttctg gagcacgggg cctgggtgac cgccaatact tgaccacccc	1147
gtcgagcccc atcgggcccgc tgcccccatg ctcgcgctgg gcagggaccg gcagccctgg	1207
aaggggcact tgatatTTTT caataaaagc ctttcgtttt gcaaaaaaaaa aaaaaaaaaa	1267
aaaaaaaaaa aaaaaaaaaa aaaaaaa	1294

<210> 16  
 <211> 220  
 <212> PRT  
 <213> homo sapiens

<400> 16

Met Ser Met Gly Leu Glu Ile Thr Gly Thr Ala Leu Ala Val Leu Gly  
 1 5 10 15

Trp Leu Gly Thr Ile Val Cys Cys Ala Leu Pro Met Trp Arg Val Ser  
 20 25 30

Ala Phe Ile Gly Ser Asn Ile Ile Thr Ser Gln Asn Ile Trp Glu Gly  
 35 40 45

Leu Trp Met Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys Lys  
 50 55 60

Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Arg  
 65 70 75 80

Ala Leu Ile Val Val Ala Ile Leu Leu Ala Ala Phe Gly Leu Leu Val  
 85 90 95

Ala Leu Val Gly Ala Gln Cys Thr Asn Cys Val Gln Asp Asp Thr Ala  
 100 105 110

Lys Ala Lys Ile Thr Ile Val Ala Gly Val Leu Phe Leu Leu Ala Ala  
 115 120 125

Leu Leu Thr Leu Val Pro Val Ser Trp Ser Ala Asn Thr Ile Ile Arg

122257 sequence listing May 10 2006.ST25.txt

130

135

140

Asp Phe Tyr Asn Pro Val Val Pro Glu Ala Gln Lys Arg Glu Met Gly  
145 150 155 160

Ala Gly Leu Tyr Val Gly Trp Ala Ala Ala Leu Gln Leu Leu Gly  
165 170 175

Gly Ala Leu Leu Cys Cys Ser Cys Pro Pro Arg Glu Lys Lys Tyr Thr  
180 185 190

Ala Thr Lys Val Val Tyr Ser Ala Pro Arg Ser Thr Gly Pro Gly Ala  
195 200 205

Ser Leu Gly Thr Gly Tyr Asp Arg Lys Asp Tyr Val  
210 215 220

<210> 17  
<211> 1853  
<212> DNA  
<213> homo sapiens

<220>  
<221> CDS  
<222> (205)..(1446)

<400> 17  
gcagtgtcac taggccggct gggggccctg ggtacgctgt agaccagacc gcgacaggcc 60  
agaacacggg cggcggcttc gggccgggag acccgcgag ccctcggggc atctcagtgc 120  
ctcactcccc accccctccc ccgggtcggg ggaggcggcg cgtccggcgg agggttgagg 180  
ggagcggggc aggcctggag cgcc atg agc agc ccg gat gcg gga tac gcc 231  
Met Ser Ser Pro Asp Ala Gly Tyr Ala  
1 5  
agt gac gac cag agc cag acc cag agc gcg ctg ccc gcg gtg atg gcc 279  
Ser Asp Asp Gln Ser Gln Thr Gln Ser Ala Leu Pro Ala Val Met Ala 25  
10 15 20  
ggg ctg ggc ccc tgc ccc tgg gcc gag tcg ctg agc ccc atc ggg gac 327  
Gly Leu Gly Pro Cys Pro Trp Ala Glu Ser Leu Ser Pro Ile Gly Asp 40  
30 35 40  
atg aag gtg aag ggc gag gcg ccg gcg aac agc gga gca ccg gcc ggg 375  
Met Lys Val Lys Gly Glu Ala Pro Ala Asn Ser Gly Ala Pro Ala Gly 55  
45 50 55  
gcc gcg ggc cga gcc aag ggc gag tcc cgt atc cgg cgg ccg atg aac 423  
Ala Ala Gly Arg Ala Lys Gly Glu Ser Arg Ile Arg Arg Pro Met Asn 60  
65 70  
gct ttc atg gtg tgg gct aag gac gag cgc aag cgg ctg gcg cag cag 471  
Ala Phe Met Val Trp Ala Lys Asp Glu Arg Lys Arg Leu Ala Gln Gln 80  
75 85  
aat cca gac ctg cac aac gcc gag ttg agc aag atg ctg ggc aag tcg 519  
Asn Pro Asp Leu His Asn Ala Glu Leu Ser Lys Met Leu Gly Lys Ser 100  
90 95 105

## 122257 sequence listing May 10 2006.ST25.txt

tgg aag gcg ctg acg ctg gcg gag aag cgg ccc ttc gtg gag gag gca Trp Lys Ala Leu Thr Leu Ala Glu Lys Arg Pro Phe Val Glu Glu Ala 110 115 120	567
gag cgg ctg cgc gtg cag cac atg cag gac cac ccc aac tac aag tac Glu Arg Leu Arg Val Gln His Met Gln Asp His Pro Asn Tyr Lys Tyr 125 130 135	615
cgg ccg cgg cgg cgc aag cag gtg aag cgg ctg aag cgg gtg gag ggc Arg Pro Arg Arg Arg Lys Gln Val Lys Arg Leu Lys Arg Val Glu Gly 140 145 150	663
ggc ttc ctg cac ggc ctg gct gag ccg cag gcg gcc gcg ctg ggc ccc Gly Phe Leu His Gly Leu Ala Glu Pro Gln Ala Ala Leu Gly Pro 155 160 165	711
gag ggc ggc cgc gtg gcc atg gac ggc ctg ggc ctc cag ttc ccc gag Glu Gly Gly Arg Val Ala Met Asp Gly Leu Gly Leu Gln Phe Pro Glu 170 175 180 185	759
cag ggc ttc ccc gcc ggc ccg ccg ctg ctg cct ccg cac atg ggc ggc Gln Gly Phe Pro Ala Gly Pro Pro Leu Leu Pro Pro His Met Gly Gly 190 195 200	807
cac tac cgc gac tgc cag agt ctg ggc gcg cct ccg ctc gac ggc tac His Tyr Arg Asp Cys Gln Ser Leu Gly Ala Pro Pro Leu Asp Gly Tyr 205 210 215	855
ccg ttg ccc acg ccc gac acg tcc ccg ctg gac ggc gtg gac ccc gac Pro Leu Pro Thr Pro Asp Thr Ser Pro Leu Asp Gly Val Asp Pro Asp 220 225 230	903
ccg gct ttc ttc gcc gcc ccg atg ccc ggg gac tgc ccg gcg gcc ggc Pro Ala Phe Phe Ala Ala Pro Met Pro Gly Asp Cys Pro Ala Ala Gly 235 240 245	951
acc tac agc tac gcg cag gtc tcg gac tac gct ggc ccc ccg gag cct Thr Tyr Ser Tyr Ala Gln Val Ser Asp Tyr Ala Gly Pro Pro Glu Pro 250 255 260 265	999
ccc gcc ggt ccc atg cac ccc cga ctc ggc cca gag ccc gcg ggt ccc Pro Ala Gly Pro Met His Pro Arg Leu Gly Pro Glu Pro Ala Gly Pro 270 275 280	1047
tcg att ccg ggc ctc ctg gcg cca ccc agc gcc ctt cac gtg tac tac Ser Ile Pro Gly Leu Leu Ala Pro Ser Ala Leu His Val Tyr Tyr 285 290 295	1095
ggc gcg atg ggc tcg ccc ggg gcg ggc ggc ggc cgc ggc ttc cag atg Gly Ala Met Gly Ser Pro Gly Ala Gly Gly Gly Arg Gly Phe Gln Met 300 305 310	1143
cag ccg caa cac cag cac cag cac cag cac cag cac cac ccc ccg ggc Gln Pro Gln His Gln His Gln His Gln His Gln His His Pro Pro Gly 315 320 325	1191
ccc gga cag ccg tcg ccc cct ccg gag gca ctg ccc tgc cgg gac ggc Pro Gly Gln Pro Ser Pro Pro Pro Glu Ala Leu Pro Cys Arg Asp Gly 330 335 340 345	1239
acg gac ccc agt cag ccc gcc gag ctc ctc ggg gag gtg gac cgc acg Thr Asp Pro Ser Gln Pro Ala Glu Leu Leu Gly Glu Val Asp Arg Thr 350 355 360	1287
gaa ttt gaa cag tat ctg cac ttc gtg tgc aag cct gag atg ggc ctc Glu Phe Glu Gln Tyr Leu His Phe Val Cys Lys Pro Glu Met Gly Leu 365 370 375	1335

122257 sequence listing May 10 2006.ST25.txt

ccc tac cag ggg cat gac tcc ggt gtg aat ctc ccc gac agc cac ggg	1383
Pro Tyr Gln Gly His Asp Ser Gly Val Asn Leu Pro Asp Ser His Gly	
380 385 390	
gcc att tcc tcg gtg gtg tcc gac gcc agc tcc gcg gta tat tac tgc	1431
Ala Ile Ser Ser Val Val Ser Asp Ala Ser Ser Ala Val Tyr Tyr Cys	
395 400 405	
aac tat cct gac gtg tgacaggtcc ctgatccgcc ccagcctgca ggccagaagc	1486
Asn Tyr Pro Asp Val	
410	
agtgttacac acttcctgga ggagctaagg aaatcctcag actcctgggt ttttgttggt	1546
gctgttggtg ttttttaaaa ggtgtgttg catataattt atggtaattt attttgtctg	1606
ccacttgaac agtttggggg ggtgaggttt cttttaaatt ttgttcagag atttgtttcc	1666
catagttgga ttgtcaaaac cctattttcca agttcaagtt aactagcttt gaatgtgtcc	1726
caaaacagct tcctccattt cctgaaagtt tattgatcaa agaaatgttg tcctgggtgt	1786
gttttttcaa tcttctaaaa aataaaatct ggaatcctga aaaaaaaaaa aaaaaaaaaa	1846
aaaaaaaa	1853

<210> 18  
 <211> 414  
 <212> PRT  
 <213> homo sapiens

<400> 18

Met Ser Ser Pro Asp Ala Gly Tyr Ala Ser Asp Asp Gln Ser Gln Thr  
 1 5 10 15

Gln Ser Ala Leu Pro Ala Val Met Ala Gly Leu Gly Pro Cys Pro Trp  
 20 25 30

Ala Glu Ser Leu Ser Pro Ile Gly Asp Met Lys Val Lys Gly Glu Ala  
 35 40 45

Pro Ala Asn Ser Gly Ala Pro Ala Gly Ala Ala Gly Arg Ala Lys Gly  
 50 55 60

Glu Ser Arg Ile Arg Arg Pro Met Asn Ala Phe Met Val Trp Ala Lys  
 65 70 75 80

Asp Glu Arg Lys Arg Leu Ala Gln Gln Asn Pro Asp Leu His Asn Ala  
 85 90 95

Glu Leu Ser Lys Met Leu Gly Lys Ser Trp Lys Ala Leu Thr Leu Ala  
 100 105 110

Glu Lys Arg Pro Phe Val Glu Glu Ala Glu Arg Leu Arg Val Gln His  
 115 120 125

Met Gln Asp His Pro Asn Tyr Lys Tyr Arg Pro Arg Arg Arg Lys Gln  
 130 135 140

122257 sequence listing May 10 2006.ST25.txt

Val Lys Arg Leu Lys Arg Val Glu Gly Gly Phe Leu His Gly Leu Ala  
145 150 155 160

Glu Pro Gln Ala Ala Ala Leu Gly Pro Glu Gly Gly Arg Val Ala Met  
165 170 175

Asp Gly Leu Gly Leu Gln Phe Pro Glu Gln Gly Phe Pro Ala Gly Pro  
180 185 190

Pro Leu Leu Pro Pro His Met Gly Gly His Tyr Arg Asp Cys Gln Ser  
195 200 205

Leu Gly Ala Pro Pro Leu Asp Gly Tyr Pro Leu Pro Thr Pro Asp Thr  
210 215 220

Ser Pro Leu Asp Gly Val Asp Pro Asp Pro Ala Phe Phe Ala Ala Pro  
225 230 235 240

Met Pro Gly Asp Cys Pro Ala Ala Gly Thr Tyr Ser Tyr Ala Gln Val  
245 250 255

Ser Asp Tyr Ala Gly Pro Pro Glu Pro Pro Ala Gly Pro Met His Pro  
260 265 270

Arg Leu Gly Pro Glu Pro Ala Gly Pro Ser Ile Pro Gly Leu Leu Ala  
275 280 285

Pro Pro Ser Ala Leu His Val Tyr Tyr Gly Ala Met Gly Ser Pro Gly  
290 295 300

Ala Gly Gly Gly Arg Gly Phe Gln Met Gln Pro Gln His Gln His Gln  
305 310 315 320

His Gln His Gln His His Pro Pro Gly Pro Gly Gln Pro Ser Pro Pro  
325 330 335

Pro Glu Ala Leu Pro Cys Arg Asp Gly Thr Asp Pro Ser Gln Pro Ala  
340 345 350

Glu Leu Leu Gly Glu Val Asp Arg Thr Glu Phe Glu Gln Tyr Leu His  
355 360 365

Phe Val Cys Lys Pro Glu Met Gly Leu Pro Tyr Gln Gly His Asp Ser  
370 375 380

Gly Val Asn Leu Pro Asp Ser His Gly Ala Ile Ser Ser Val Val Ser  
385 390 395 400

Asp Ala Ser Ser Ala Val Tyr Tyr Cys Asn Tyr Pro Asp Val  
405 410

## 122257 sequence listing May 10 2006.ST25.txt

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<210> 19
<211> 3702
<212> DNA
<213> homo sapiens
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<220>
<221> CDS
<222> (159) .. (2237)
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<400>	19															
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acctccacct	cccgggttca	agtgattctc	atgcctcagc	ctcccagagta	gctgggatta	120										
caggtggtga	cttccaagag	tgactccgtc	ggaggaaa	atg	act	ccc	cag	tcg	ctg	176						
				Met	Thr	Pro	Gln	Ser	Leu							
				1				5								
ctg	cag	acg	aca	ctg	ttc	ctg	ctg	agt	ctg	ctc	ttc	ctg	gtc	caa	ggt	224
Leu	Gln	Thr	Thr	Leu	Phe	Leu	Leu	Ser	Leu	Leu	Phe	Leu	Val	Gln	Gly	
			10					15					20			
gcc	cac	ggc	agg	ggc	cac	agg	gaa	gac	ttt	cgc	ttc	tgc	agc	cag	cgg	272
Ala	His	Gly	Arg	Gly	His	Arg	Glu	Asp	Phe	Arg	Phe	Cys	Ser	Gln	Arg	
		25					30					35				
aac	cag	aca	cac	agg	agc	agc	ctc	cac	tac	aaa	ccc	aca	cca	gac	ctg	320
Asn	Gln	Thr	His	Arg	Ser	Ser	Leu	His	Tyr	Lys	Pro	Thr	Pro	Asp	Leu	
	40					45					50					
cgc	atc	tcc	atc	gag	aac	tcc	gaa	gag	gcc	ctc	aca	gtc	cat	gcc	cct	368
Arg	Ile	Ser	Ile	Glu	Asn	Ser	Glu	Glu	Ala	Leu	Thr	Val	His	Ala	Pro	
					60					65					70	
ttc	cct	gca	gcc	cac	cct	gct	tcc	cga	tcc	ttc	cct	gac	ccc	agg	ggc	416
Phe	Pro	Ala	Ala	His	Pro	Ala	Ser	Arg	Ser	Phe	Pro	Asp	Pro	Arg	Gly	
				75					80					85		
ctc	tac	cac	ttc	tgc	ctc	tac	tgg	aac	cga	cat	gct	ggg	aga	tta	cat	464
Leu	Tyr	His	Phe	Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	
			90					95					100			
ctt	ctc	tat	ggc	aag	cgt	gac	ttc	ttg	ctg	agt	gac	aaa	gcc	tct	agc	512
Leu	Leu	Tyr	Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	
		105					110					115				
ctc	ctc	tgc	ttc	cag	cac	cag	gag	gag	agc	ctg	gct	cag	ggc	ccc	ccg	560
Leu	Leu	Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	
	120					125					130					
ctg	tta	gcc	act	tct	gtc	acc	tcc	tgg	tgg	agc	cct	cag	aac	atc	agc	608
Leu	Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	
					140					145					150	
ctg	ccc	agt	gcc	gcc	agc	ttc	acc	ttc	tcc	ttc	cac	agt	cct	ccc	cac	656
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	His	
				155					160					165		
acg	gcc	gct	cac	aat	gcc	tcg	gtg	gac	atg	tgc	gag	ctc	aaa	agg	gac	704
Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	Arg	Asp	
			170					175					180			
ctc	cag	ctg	ctc	agc	cag	ttc	ctg	aag	cat	ccc	cag	aag	gcc	tca	agg	752
Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	Ala	Ser	Arg	
		185					190					195				

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agg	ccc	tcg	gct	gcc	ccc	gcc	agc	cag	cag	ttg	cag	agc	ctg	gag	tcg	800
Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	Ser	Leu	Glu	Ser	
	200					205					210					
aaa	ctg	acc	tct	gtg	aga	ttc	atg	ggg	gac	atg	gtg	tcc	ttc	gag	gag	848
Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	Val	Ser	Phe	Glu	Glu	
215					220					225					230	
gac	cgg	atc	aac	gcc	acg	gtg	tgg	aag	ctc	cag	ccc	aca	gcc	ggc	ctc	896
Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	Gln	Pro	Thr	Ala	Gly	Leu	
				235					240					245		
cag	gac	ctg	cac	atc	cac	tcc	cgg	cag	gag	gag	gag	cag	agc	gag	atc	944
Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	Glu	Glu	Glu	Gln	Ser	Glu	Ile	
			250					255					260			
atg	gag	tac	tcg	gtg	ctg	ctg	cct	cga	aca	ctc	ttc	cag	agg	acg	aaa	992
Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	
		265					270					275				
ggc	cgg	agc	ggg	gag	gct	gag	aag	aga	ctc	ctc	ctg	gtg	gac	ttc	agc	1040
Gly	Arg	Ser	Gly	Glu	Ala	Glu	Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	
	280					285					290					
agc	caa	gcc	ctg	ttc	cag	gac	aag	aat	tcc	agc	cac	gtc	ctg	ggt	gag	1088
Ser	Gln	Ala	Leu	Phe	Gln	Asp	Lys	Asn	Ser	Ser	His	Val	Leu	Gly	Glu	
295					300					305					310	
aag	gtc	ttg	ggg	att	gtg	gta	cag	aac	acc	aaa	gta	gcc	aac	ctc	acg	1136
Lys	Val	Leu	Gly	Ile	Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	
				315					320					325		
gag	ccc	gtg	gtg	ctc	acc	ttc	cag	cac	cag	cta	cag	ccg	aag	aat	gtg	1184
Glu	Pro	Val	Val	Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	
			330					335					340			
act	ctg	caa	tgt	gtg	ttc	tgg	gtt	gaa	gac	ccc	aca	ttg	agc	agc	ccg	1232
Thr	Leu	Gln	Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	
		345					350					355				
ggg	cat	tgg	agc	agt	gct	ggg	tgt	gag	acc	gtc	agg	aga	gaa	acc	caa	1280
Gly	His	Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	
	360					365					370					
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Thr	Ser	Cys	Phe	Cys	Asn	His	Leu	Thr	Tyr	Phe	Ala	Val	Leu	Met	Val	
375					380					385					390	
tcc	tcg	gtg	gag	gtg	gac	gcc	gtg	cac	aag	cac	tac	ctg	agc	ctc	ctc	1376
Ser	Ser	Val	Glu	Val	Asp	Ala	Val	His	Lys	His	Tyr	Leu	Ser	Leu	Leu	
				395					400					405		
tcc	tac	gtg	ggc	tgt	gtc	gtc	tct	gcc	ctg	gcc	tgc	ctt	gtc	acc	att	1424
Ser	Tyr	Val	Gly	Cys	Val	Val	Ser	Ala	Leu	Ala	Cys	Leu	Val	Thr	Ile	
			410					415					420			
gcc	gcc	tac	ctc	tgc	tcc	agg	gtg	ccc	ctg	ccg	tgc	agg	agg	aaa	cct	1472
Ala	Ala	Tyr	Leu	Cys	Ser	Arg	Val	Pro	Leu	Pro	Cys	Arg	Arg	Lys	Pro	
		425					430					435				
cgg	gac	tac	acc	atc	aag	gtg	cac	atg	aac	ctg	ctg	ctg	gcc	gtc	ttc	1520
Arg	Asp	Tyr	Thr	Ile	Lys	Val	His	Met	Asn	Leu	Leu	Leu	Ala	Val	Phe	
	440					445					450					
ctg	ctg	gac	acg	agc	ttc	ctg	ctc	agc	gag	ccg	gtg	gcc	ctg	aca	ggc	1568
Leu	Leu	Asp	Thr	Ser	Phe	Leu	Leu	Ser	Glu	Pro	Val	Ala	Leu	Thr	Gly	
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tct gag gct ggc tgc cga gcc agt gcc atc ttc ctg cac ttc tcc ctg	1616
Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile Phe Leu His Phe Ser Leu	
475 480 485	
ctc acc tgc ctt tcc tgg atg ggc ctc gag ggg tac aac ctc tac cga	1664
Leu Thr Cys Leu Ser Trp Met Gly Leu Glu Gly Tyr Asn Leu Tyr Arg	
490 495 500	
ctc gtg gtg gag gtc ttt ggc acc tat gtc cct ggc tac cta ctc aag	1712
Leu Val Val Glu Val Phe Gly Thr Tyr Val Pro Gly Tyr Leu Leu Lys	
505 510 515	
ctg agc gcc atg ggc tgg ggc ttc ccc atc ttt ctg gtg acg ctg gtg	1760
Leu Ser Ala Met Gly Trp Gly Phe Pro Ile Phe Leu Val Thr Leu Val	
520 525 530	
gcc ctg gtg gat gtg gac aac tat ggc ccc atc atc ttg gct gtg cat	1808
Ala Leu Val Asp Val Asp Asn Tyr Gly Pro Ile Ile Leu Ala Val His	
535 540 545 550	
agg act cca gag ggc gtc atc tac cct tcc atg tgc tgg atc cgg gac	1856
Arg Thr Pro Glu Gly Val Ile Tyr Pro Ser Met Cys Trp Ile Arg Asp	
555 560 565	
tcc ctg gtc agc tac atc acc aac ctg ggc ctc ttc agc ctg gtg ttt	1904
Ser Leu Val Ser Tyr Ile Thr Asn Leu Gly Leu Phe Ser Leu Val Phe	
570 575 580	
ctg ttc aac atg gcc atg cta gcc acc atg gtg gtg cag atc ctg cgg	1952
Leu Phe Asn Met Ala Met Leu Ala Thr Met Val Val Gln Ile Leu Arg	
585 590 595	
ctg cgc ccc cac acc caa aag tgg tca cat gtg ctg aca ctg ctg ggc	2000
Leu Arg Pro His Thr Gln Lys Trp Ser His Val Leu Thr Leu Leu Gly	
600 605 610	
ctc agc ctg gtc ctt ggc ctg ccc tgg gcc ttg atc ttc ttc tcc ttt	2048
Leu Ser Leu Val Leu Gly Leu Pro Trp Ala Leu Ile Phe Phe Ser Phe	
615 620 625 630	
gct tct ggc acc ttc cag ctt gtc gtc ctc tac ctt ttc agc atc atc	2096
Ala Ser Gly Thr Phe Gln Leu Val Val Leu Tyr Leu Phe Ser Ile Ile	
635 640 645	
acc tcc ttc caa ggc ttc ctc atc ttc atc tgg tac tgg tcc atg cgg	2144
Thr Ser Phe Gln Gly Phe Leu Ile Phe Ile Trp Tyr Trp Ser Met Arg	
650 655 660	
ctg cag gcc cgg ggt ggc ccc tcc cct ctg aag agc aac tca gac agc	2192
Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn Ser Asp Ser	
665 670 675	
gcc agg ctc ccc atc agc tcg ggc agc acc tcg tcc agc cgc atc	2237
Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser Ser Arg Ile	
680 685 690	
taggcctcca gcccacctgc ccatgtgatg aagcagagat gcggcctcgt cgcacactgc	2297
ctgtggcccc cgagccaggc ccagccccag gccagtcagc cgcagacttt ggaaagccca	2357
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ttacaaaccc tgggcccagc cctcattgct gggggccagg ccttggatct tgagggtctg	2597



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```

gcacatcctt aatcctgtgc ccctgcctgg gacagaaatg tggctccagt tgctctgtct 2657
ctcgtgggtca ccctgagggc actctgcatc ctctgtcatt ttaacctcag gtggcaccca 2717
gggcgaatgg ggcccagggc agaccttcag ggccagagcc ctggcggagg agaggccctt 2777
tgccaggagc acagcagcag ctgcctacc tctgagccca ggccccctcc ctccctcagc 2837
ccccagttcc tccctccatc ttccctgggg ttctctctct ctcccagggc ctcccttgctc 2897
cttcgttcac agctgggggt ccccgattcc aatgctgttt tttggggagt ggtttccagg 2957
agctgcctgg tgtctgtgt aaatgtttgt ctactgcaca agcctcggcc tgcccctgag 3017
ccaggctcgg taccgatgcg tgggctgggc taggtccctc tgtccatctg ggcctttgta 3077
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ggttaattct gtccaacaaa cacacacggg tagattgctg gcctgttgta ggtggtaggg 3377
acacagatga ccgacctggc cactcctcct gccaacattc agtctggtat gtgaggcgtg 3437
cgtgaagcaa gaactcctgg agctacaggg acagggagcc atcattcctg cctgggaatc 3497
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ctttttacgt accaattctt ttgtcttttg atattaaaaa gaagtacatg ttcatgtag 3617
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cctagcaaaa aaaaaaaaaa aaaaa 3702

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<210> 20
<211> 693
<212> PRT
<213> homo sapiens

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<400> 20

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Met Thr Pro Gln Ser Leu Leu Gln Thr Thr Leu Phe Leu Leu Ser Leu
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Leu Phe Leu Val Gln Gly Ala His Gly Arg Gly His Arg Glu Asp Phe
          20          25          30

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```

Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser Leu His Tyr
          35          40          45

```

```

Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn Ser Glu Glu Ala
          50          55          60

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Leu Thr Val His Ala Pro Phe Pro Ala Ala His Pro Ala Ser Arg Ser
65          70          75          80

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Phe Pro Asp Pro Arg Gly Leu Tyr His Phe Cys Leu Tyr Trp Asn Arg

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His Ala Gly Arg Leu His Leu Leu Tyr Gly Lys Arg Asp Phe Leu Leu  
100 105 110

Ser Asp Lys Ala Ser Ser Leu Leu Cys Phe Gln His Gln Glu Glu Ser  
115 120 125

Leu Ala Gln Gly Pro Pro Leu Leu Ala Thr Ser Val Thr Ser Trp Trp  
130 135 140

Ser Pro Gln Asn Ile Ser Leu Pro Ser Ala Ala Ser Phe Thr Phe Ser  
145 150 155 160

Phe His Ser Pro Pro His Thr Ala Ala His Asn Ala Ser Val Asp Met  
165 170 175

Cys Glu Leu Lys Arg Asp Leu Gln Leu Leu Ser Gln Phe Leu Lys His  
180 185 190

Pro Gln Lys Ala Ser Arg Arg Pro Ser Ala Ala Pro Ala Ser Gln Gln  
195 200 205

Leu Gln Ser Leu Glu Ser Lys Leu Thr Ser Val Arg Phe Met Gly Asp  
210 215 220

Met Val Ser Phe Glu Glu Asp Arg Ile Asn Ala Thr Val Trp Lys Leu  
225 230 235 240

Gln Pro Thr Ala Gly Leu Gln Asp Leu His Ile His Ser Arg Gln Glu  
245 250 255

Glu Glu Gln Ser Glu Ile Met Glu Tyr Ser Val Leu Leu Pro Arg Thr  
260 265 270

Leu Phe Gln Arg Thr Lys Gly Arg Ser Gly Glu Ala Glu Lys Arg Leu  
275 280 285

Leu Leu Val Asp Phe Ser Ser Gln Ala Leu Phe Gln Asp Lys Asn Ser  
290 295 300

Ser His Val Leu Gly Glu Lys Val Leu Gly Ile Val Val Gln Asn Thr  
305 310 315 320

Lys Val Ala Asn Leu Thr Glu Pro Val Val Leu Thr Phe Gln His Gln  
325 330 335

Leu Gln Pro Lys Asn Val Thr Leu Gln Cys Val Phe Trp Val Glu Asp  
340 345 350

Pro Thr Leu Ser Ser Pro Gly His Trp Ser Ser Ala Gly Cys Glu Thr

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355

360

365

Val Arg Arg Glu Thr Gln Thr Ser Cys Phe Cys Asn His Leu Thr Tyr  
 370 375 380

Phe Ala Val Leu Met Val Ser Ser Val Glu Val Asp Ala Val His Lys  
 385 390 395 400

His Tyr Leu Ser Leu Leu Ser Tyr Val Gly Cys Val Val Ser Ala Leu  
 405 410 415

Ala Cys Leu Val Thr Ile Ala Ala Tyr Leu Cys Ser Arg Val Pro Leu  
 420 425 430

Pro Cys Arg Arg Lys Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn  
 435 440 445

Leu Leu Leu Ala Val Phe Leu Leu Asp Thr Ser Phe Leu Leu Ser Glu  
 450 455 460

Pro Val Ala Leu Thr Gly Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile  
 465 470 475 480

Phe Leu His Phe Ser Leu Leu Thr Cys Leu Ser Trp Met Gly Leu Glu  
 485 490 495

Gly Tyr Asn Leu Tyr Arg Leu Val Val Glu Val Phe Gly Thr Tyr Val  
 500 505 510

Pro Gly Tyr Leu Leu Lys Leu Ser Ala Met Gly Trp Gly Phe Pro Ile  
 515 520 525

Phe Leu Val Thr Leu Val Ala Leu Val Asp Val Asp Asn Tyr Gly Pro  
 530 535 540

Ile Ile Leu Ala Val His Arg Thr Pro Glu Gly Val Ile Tyr Pro Ser  
 545 550 555 560

Met Cys Trp Ile Arg Asp Ser Leu Val Ser Tyr Ile Thr Asn Leu Gly  
 565 570 575

Leu Phe Ser Leu Val Phe Leu Phe Asn Met Ala Met Leu Ala Thr Met  
 580 585 590

Val Val Gln Ile Leu Arg Leu Arg Pro His Thr Gln Lys Trp Ser His  
 595 600 605

Val Leu Thr Leu Leu Gly Leu Ser Leu Val Leu Gly Leu Pro Trp Ala  
 610 615 620

Leu Ile Phe Phe Ser Phe Ala Ser Gly Thr Phe Gln Leu Val Val Leu  
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625 630 635 640

Tyr Leu Phe Ser Ile Ile Thr Ser Phe Gln Gly Phe Leu Ile Phe Ile  
645 650 655

Trp Tyr Trp Ser Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu  
660 665 670

Lys Ser Asn Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr  
675 680 685

Ser Ser Ser Arg Ile  
690

<210> 21  
<211> 1332  
<212> DNA  
<213> homo sapiens

<220>  
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<222> (427)..(1059)

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tgcctagggt cgccgagagc gcccggaggg aaccgccttg ccttcgggga ccaccaattt 180  
tgtctggaac caccctcccg gcgtatccta ctccctgtgc cgcgaggcca tcgcttcact 240  
ggaggggtcg atttgtgtgt agtttggtga caagatttgc attcacctgg cccaaaccct 300  
ttttgtctct ttgggtgacc ggaaaactcc acctcaagtt ttctttttgtg gggctgcccc 360  
ccaagtgtcg tttgttttac ttaggggtct cccgcccggc gccccagtg ttttctgagg 420  
gcggaa atg gcc aat tcg ggc ctg cag ttg ctg ggc ttc tcc atg gcc 468  
Met Ala Asn Ser Gly Leu Gln Leu Leu Gly Phe Ser Met Ala  
1 5 10  
ctg ctg ggc tgg gtg ggt ctg gtg gcc tgc acc gcc atc ccg cag tgg 516  
Leu Leu Gly Trp Val Gly Leu Val Ala Cys Thr Ala Ile Pro Gln Trp  
15 20 25 30  
cag atg agc tcc tat gcg ggt gac aac atc atc acg gcc cag gcc atg 564  
Gln Met Ser Ser Tyr Ala Gly Asp Asn Ile Ile Thr Ala Gln Ala Met  
35 40 45  
tac aag ggg ctg tgg atg gac tgc gtc acg cag agc acg ggg atg atg 612  
Tyr Lys Gly Leu Trp Met Asp Cys Val Thr Gln Ser Thr Gly Met Met  
50 55 60  
agc tgc aaa atg tac gac tcg gtg ctc gcc ctg tcc gcg gcc ttg cag 660  
Ser Cys Lys Met Tyr Asp Ser Val Leu Ala Leu Ser Ala Ala Leu Gln  
65 70 75  
gcc act cga gcc cta atg gtg gtc tcc ctg gtg ctg ggc ttc ctg gcc 708  
Ala Thr Arg Ala Leu Met Val Val Ser Leu Val Leu Gly Phe Leu Ala  
80 85 90

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atg ttt gtg gcc acg atg ggc atg aag tgc acg cgc tgt ggg gga gac Met Phe Val Ala Thr Met Gly Met Lys Cys Thr Arg Cys Gly Gly Asp 95 100 105 110	756
gac aaa gtg aag aag gcc cgt ata gcc atg ggt gga ggc ata att ttc Asp Lys Val Lys Lys Ala Arg Ile Ala Met Gly Gly Gly Ile Ile Phe 115 120 125	804
atc gtg gca ggt ctt gcc acc ttg gta gct tgc tcc tgg tat ggc cat Ile Val Ala Gly Leu Ala Thr Leu Val Ala Cys Ser Trp Tyr Gly His 130 135 140	852
cag att gtc aca gac ttt tat aac cct ttg atc cct acc aac att aag Gln Ile Val Thr Asp Phe Tyr Asn Pro Leu Ile Pro Thr Asn Ile Lys 145 150 155	900
tat gag ttt ggc cct gcc atc ttt att ggc tgg gca ggg tct gcc cta Tyr Glu Phe Gly Pro Ala Ile Phe Ile Gly Trp Ala Gly Ser Ala Leu 160 165 170	948
gtc atc ctg gga ggt gca ctg ctc tcc tgt tcc tgt cct ggg aat gag Val Ile Leu Gly Gly Ala Leu Leu Ser Cys Ser Cys Pro Gly Asn Glu 175 180 185 190	996
agc aag gct ggg tac cgt gca ccc cgc tct tac cct aag tcc aac tct Ser Lys Ala Gly Tyr Arg Ala Pro Arg Ser Tyr Pro Lys Ser Asn Ser 195 200 205	1044
tcc aag gag tat gtg tgacctggga tctccttgcc ccagcctgac aggctatggg Ser Lys Glu Tyr Val 210	1099
agtgtctaga tgcctgaaag ggcctggggc tgagctcagc ctgtgggcag ggtgccggac	1159
aaaggcctcc tggtcactct gtccctgcac tccatgtata gtcctcttgg gttgggggtg	1219
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Ser Ser Tyr Ala Gly Asp Asn Ile Ile Thr Ala Gln Ala Met Tyr Lys 35 40 45	
Gly Leu Trp Met Asp Cys Val Thr Gln Ser Thr Gly Met Met Ser Cys 50 55 60	
Lys Met Tyr Asp Ser Val Leu Ala Leu Ser Ala Ala Leu Gln Ala Thr 65 70 75 80	

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ttg caa aaa gga att gga gaa ttc ttt agg ttg tcc cct aaa gat tct 302  
 Trp Gln Lys Gly Ile Gly Glu Phe Phe Arg Leu Ser Pro Lys Asp Ser  
                     65                    70                    75

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gaa aaa gag aat cag att cct gaa gag gca gga agc agt ggc tta gga	350
Glu Lys Glu Asn Gln Ile Pro Glu Glu Ala Gly Ser Ser Gly Leu Gly	
80 85 90	
aaa gca aag aga aaa gca tgt cct ttg caa cct gat cac aca aat gat	398
Lys Ala Lys Arg Lys Ala Cys Pro Leu Gln Pro Asp His Thr Asn Asp	
95 100 105	
gaa aaa gaa tagaactttc tcattcatct ttgaataacg tctccttgtt	447
Glu Lys Glu	
110	
taccctggta ttctagaatg taaattttaca taaatgtgtt tgttccaatt agctttgttg	507
aacaggcatt taattaaaaa atttaggttt aaatttagat gttcaaaagt agttgtgaaa	567
tttgagaatt tgtaagacta attatggtaa cttagcttag tattcaatat aatgcattgt	627
ttggtttctt ttaccaaatt aagtgtctag ttcttgctaa aatcaagtca ttgcattgtg	687
ttctaattac aagtatgttg tatttgagat ttgcttagat tgttgtactg ctgccatttt	747
tattggtgtt tgattattgg aatggtgcc aattgtcact ctttctactt gctttaaaaa	807
gcagagttag atttttgcac attaaaaaaa ttcagtatta attaaacact aaaaaaaaaa	867
aaaaaaaaa aaaaaaaaaa a	888

<210> 24  
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 <212> PRT  
 <213> homo sapiens  
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Thr Asn Ser Thr Ser Val Ser Ser Arg Lys Ala Glu Asn Lys Tyr Ala
35 40 45
Gly Gly Asn Pro Val Cys Val Arg Pro Thr Pro Lys Trp Gln Lys Gly
50 55 60
Ile Gly Glu Phe Phe Arg Leu Ser Pro Lys Asp Ser Glu Lys Glu Asn
65 70 75 80
Gln Ile Pro Glu Glu Ala Gly Ser Ser Gly Leu Gly Lys Ala Lys Arg
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Lys Ala Cys Pro Leu Gln Pro Asp His Thr Asn Asp Glu Lys Glu
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<210> 25  
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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (23)..(418)

&lt;400&gt; 25

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                        1          5          10

gtg ctg ctt gcc ctg gga act ctg gca cct tgg gct gtg gaa ggc tct      100
Val Leu Leu Ala Leu Gly Thr Leu Ala Pro Trp Ala Val Glu Gly Ser
                        15          20          25

gga aag tcc ttc aaa gct gga gtc tgt cct cct aag aaa tct gcc cag      148
Gly Lys Ser Phe Lys Ala Gly Val Cys Pro Pro Lys Lys Ser Ala Gln
                        30          35          40

tgc ctt aga tac aag aaa cct gag tgc cag agt gac tgg cag tgt cca      196
Cys Leu Arg Tyr Lys Lys Pro Glu Cys Gln Ser Asp Trp Gln Cys Pro
                        45          50          55

ggg aag aag aga tgt tgt cct gac act tgt ggc atc aaa tgc ctg gat      244
Gly Lys Lys Arg Cys Cys Pro Asp Thr Cys Gly Ile Lys Cys Leu Asp
                        60          65          70

cct gtt gac acc cca aac cca aca agg agg aag cct ggg aag tgc cca      292
Pro Val Asp Thr Pro Asn Pro Thr Arg Arg Lys Pro Gly Lys Cys Pro
                        75          80          85

gtg act tat ggc caa tgt ttg atg ctt aac ccc ccc aat ttc tgt gag      340
Val Thr Tyr Gly Gln Cys Leu Met Leu Asn Pro Pro Asn Phe Cys Glu
                        95          100          105

atg gat ggc cag tgc aag cgt gac ttg aag tgt tgc atg ggc atg tgt      388
Met Asp Gly Gln Cys Lys Arg Asp Leu Lys Cys Cys Met Gly Met Cys
                        110          115          120

ggg aaa tcc tgc gtt tcc cct gtg aaa gct tgattcctgc catatggagg      438
Gly Lys Ser Cys Val Ser Pro Val Lys Ala
                        125          130

aggctctgga gtcctgctct gtgtgggtcca ggtcctttcc accctgagac ttggctccac      498

cactgatatc ctcttttggg gaaaggcttg gcacacagca ggctttcaag aagtgccagt      558

tgatcaatga ataaataaac gaggcctatct ctctttgcac      598

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&lt;210&gt; 26

&lt;211&gt; 132

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 26

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Met Lys Ser Ser Gly Leu Phe Pro Phe Leu Val Leu Leu Ala Leu Gly
1          5          10          15

Thr Leu Ala Pro Trp Ala Val Glu Gly Ser Gly Lys Ser Phe Lys Ala
20          25          30

Gly Val Cys Pro Pro Lys Lys Ser Ala Gln Cys Leu Arg Tyr Lys Lys
35          40          45

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Pro Glu Cys Gln Ser Asp Trp Gln Cys Pro Gly Lys Lys Arg Cys Cys  
50 55 60

Pro Asp Thr Cys Gly Ile Lys Cys Leu Asp Pro Val Asp Thr Pro Asn  
65 70 75 80

Pro Thr Arg Arg Lys Pro Gly Lys Cys Pro Val Thr Tyr Gly Gln Cys  
85 90 95

Leu Met Leu Asn Pro Pro Asn Phe Cys Glu Met Asp Gly Gln Cys Lys  
100 105 110

Arg Asp Leu Lys Cys Cys Met Gly Met Cys Gly Lys Ser Cys Val Ser  
115 120 125

Pro Val Lys Ala  
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ggccagtgtc tggcacaggg gaagcattct aaaaatatag ctgatgctgt taaacaatga 180  
ctgttggtgt tgttttactg ttattatccc caaagcggcc cattctgtct gttgctgtca 240  
gctatgactc agtccccctga ttaacttacg caccacccat tttatcccct gcagagatgc 300  
tgccccacc cccttaggcc cgagggatca ggagct atg gga cca gag gcc ctg 354  
Met Gly Pro Glu Ala Leu  
1 5  
tca tct tta ctg ctg ctg ctc ttg gtg gca agt gga gat gct gac atg 402  
Ser Ser Leu Leu Leu Leu Leu Val Ala Ser Gly Asp Ala Asp Met  
10 15 20  
aag gga cat ttt gat cct gcc aag tgc cgc tat gcc ctg ggc atg cag 450  
Lys Gly His Phe Asp Pro Ala Lys Cys Arg Tyr Ala Leu Gly Met Gln  
25 30 35  
gac cgg acc atc cca gac agt gac atc tct gct tcc agc tcc tgg tca 498  
Asp Arg Thr Ile Pro Asp Ser Asp Ile Ser Ala Ser Ser Ser Trp Ser  
40 45 50  
gat tcc act gcc gcc cgc cac agc agg ttg gag agc agt gac ggg gat 546  
Asp Ser Thr Ala Ala Arg His Ser Arg Leu Glu Ser Ser Asp Gly Asp  
55 60 65 70  
ggg gcc tgg tgc ccc gca ggg tcg gtg ttt ccc aag gag gag gag tac 594

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Gly	Ala	Trp	Cys	Pro	Ala	Gly	Ser	Val	Phe	Pro	Lys	Glu	Glu	Glu	Tyr	
				75					80					85		
ttg	cag	gtg	gat	cta	caa	cga	ctg	cac	ctg	gtg	gct	ctg	gtg	ggc	acc	642
Leu	Gln	Val	Asp	Leu	Gln	Arg	Leu	His	Leu	Val	Ala	Leu	Val	Gly	Thr	
			90					95					100			
cag	gga	cgg	cat	gcc	ggg	ggc	ctg	ggc	aag	gag	ttc	tcc	cgg	agc	tac	690
Gln	Gly	Arg	His	Ala	Gly	Gly	Leu	Gly	Lys	Glu	Phe	Ser	Arg	Ser	Tyr	
		105					110					115				
cgg	ctg	cgt	tac	tcc	cgg	gat	ggg	cgc	cgc	tgg	atg	ggc	tgg	aag	gac	738
Arg	Leu	Arg	Tyr	Ser	Arg	Asp	Gly	Arg	Arg	Trp	Met	Gly	Trp	Lys	Asp	
	120					125					130					
cgc	tgg	ggt	cag	gag	gtg	atc	tca	ggc	aat	gag	gac	cct	gag	gga	gtg	786
Arg	Trp	Gly	Gln	Glu	Val	Ile	Ser	Gly	Asn	Glu	Asp	Pro	Glu	Gly	Val	
					140					145					150	
gtg	ctg	aag	gac	ctt	ggg	ccc	ccc	atg	gtt	gcc	cga	ctg	gtt	cgc	ttc	834
Val	Leu	Lys	Asp	Leu	Gly	Pro	Pro	Met	Val	Ala	Arg	Leu	Val	Arg	Phe	
				155					160					165		
tac	ccc	cgg	gct	gac	cgg	gtc	atg	agc	gtc	tgt	ctg	cgg	gta	gag	ctc	882
Tyr	Pro	Arg	Ala	Asp	Arg	Val	Met	Ser	Val	Cys	Leu	Arg	Val	Glu	Leu	
			170					175					180			
tat	ggc	tgc	ctc	tgg	agg	gat	gga	ctc	ctg	tct	tac	acc	gcc	cct	gtg	930
Tyr	Gly	Cys	Leu	Trp	Arg	Asp	Gly	Leu	Leu	Ser	Tyr	Thr	Ala	Pro	Val	
		185					190					195				
ggg	cag	aca	atg	tat	tta	tct	gag	gcc	gtg	tac	ctc	aac	gac	tcc	acc	978
Gly	Gln	Thr	Met	Tyr	Leu	Ser	Glu	Ala	Val	Tyr	Leu	Asn	Asp	Ser	Thr	
	200					205					210					
tat	gac	gga	cat	acc	gtg	ggc	gga	ctg	cag	tat	ggg	ggt	ctg	ggc	cag	1026
Tyr	Asp	Gly	His	Thr	Val	Gly	Gly	Leu	Gln	Tyr	Gly	Gly	Leu	Gly	Gln	
					220					225					230	
ctg	gca	gat	ggt	gtg	gtg	ggg	ctg	gat	gac	ttt	agg	aag	agt	cag	gag	1074
Leu	Ala	Asp	Gly	Val	Val	Gly	Leu	Asp	Asp	Phe	Arg	Lys	Ser	Gln	Glu	
				235					240					245		
ctg	cgg	gtc	tgg	cca	ggc	tat	gac	tat	gtg	gga	tgg	agc	aac	cac	agc	1122
Leu	Arg	Val	Trp	Pro	Gly	Tyr	Asp	Tyr	Val	Gly	Trp	Ser	Asn	His	Ser	
			250				255						260			
ttc	tcc	agt	ggc	tat	gtg	gag	atg	gag	ttt	gag	ttt	gac	cgg	ctg	agg	1170
Phe	Ser	Ser	Gly	Tyr	Val	Glu	Met	Glu	Phe	Glu	Phe	Asp	Arg	Leu	Arg	
		265					270					275				
gcc	ttc	cag	gct	atg	cag	gtc	cac	tgt	aac	aac	atg	cac	acg	ctg	gga	1218
Ala	Phe	Gln	Ala	Met	Gln	Val	His	Cys	Asn	Asn	Met	His	Thr	Leu	Gly	
	280					285					290					
gcc	cgt	ctg	cct	ggc	ggg	gtg	gaa	tgt	cgc	ttc	cgg	cgt	ggc	cct	gcc	1266
Ala	Arg	Leu	Pro	Gly	Gly	Val	Glu	Cys	Arg	Phe	Arg	Arg	Gly	Pro	Ala	
					300					305					310	
atg	gcc	tgg	gag	ggg	gag	ccc	atg	cgc	cac	aac	cta	ggg	ggc	aac	ctg	1314
Met	Ala	Trp	Glu	Gly	Glu	Pro	Met	Arg	His	Asn	Leu	Gly	Gly	Asn	Leu	
				315					320					325		
ggg	gac	ccc	aga	gcc	cgg	gct	gtc	tca	gtg	ccc	ctt	ggc	ggc	cgt	gtg	1362
Gly	Asp	Pro	Arg	Ala	Arg	Ala	Val	Ser	Val	Pro	Leu	Gly	Gly	Arg	Val	
			330					335					340			
gct	cgc	ttt	ctg	cag	tgc	cgc	ttc	ctc	ttt	gcg	ggg	ccc	tgg	tta	ctc	1410

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Ala	Arg	Phe	Leu	Gln	Cys	Arg	Phe	Leu	Phe	Ala	Gly	Pro	Trp	Leu	Leu	
		345					350					355				
ttc	agc	gaa	atc	tcc	ttc	atc	tct	gat	gtg	gtg	aac	aat	tcc	tct	ccg	1458
Phe	Ser	Glu	Ile	Ser	Phe	Ile	Ser	Asp	Val	Val	Asn	Asn	Ser	Ser	Pro	
	360					365					370					
gca	ctg	gga	ggc	acc	ttc	ccg	cca	gcc	ccc	tgg	tgg	ccg	cct	ggc	cca	1506
Ala	Leu	Gly	Gly	Thr	Phe	Pro	Pro	Ala	Pro	Trp	Trp	Pro	Pro	Gly	Pro	
375					380					385					390	
cct	ccc	acc	aac	ttc	agc	agc	ttg	gag	ctg	gag	ccc	aga	ggc	cag	cag	1554
Pro	Pro	Thr	Asn	Phe	Ser	Ser	Leu	Glu	Leu	Glu	Pro	Arg	Gly	Gln	Gln	
				395					400					405		
ccc	gtg	gcc	aag	gcc	gag	ggg	agc	ccg	acc	gcc	atc	ctc	atc	ggc	tgc	1602
Pro	Val	Ala	Lys	Ala	Glu	Gly	Ser	Pro	Thr	Ala	Ile	Leu	Ile	Gly	Cys	
			410					415					420			
ctg	gtg	gcc	atc	atc	ctg	ctc	ctg	ctg	ctc	atc	att	gcc	ctc	atg	ctc	1650
Leu	Val	Ala	Ile	Ile	Leu	Leu	Leu	Leu	Leu	Ile	Ile	Ala	Leu	Met	Leu	
		425				430						435				
tgg	cgg	ctg	cac	tgg	cgc	agg	ctc	ctc	agc	aag	gct	gaa	cgg	agg	gtg	1698
Trp	Arg	Leu	His	Trp	Arg	Arg	Leu	Leu	Ser	Lys	Ala	Glu	Arg	Arg	Val	
	440					445					450					
ttg	gaa	gag	gag	ctg	acg	gtt	cac	ctc	tct	gtc	cct	ggg	gac	act	atc	1746
Leu	Glu	Glu	Glu	Leu	Thr	Val	His	Leu	Ser	Val	Pro	Gly	Asp	Thr	Ile	
455					460					465					470	
ctc	atc	aac	aac	cgc	cca	ggt	cct	aga	gag	cca	ccc	ccg	tac	cag	gag	1794
Leu	Ile	Asn	Asn	Arg	Pro	Gly	Pro	Arg	Glu	Pro	Pro	Pro	Tyr	Gln	Glu	
				475					480					485		
ccc	cgg	cct	cgt	ggg	aat	ccg	ccc	cac	tcc	gct	ccc	tgt	gtc	ccc	aat	1842
Pro	Arg	Pro	Arg	Gly	Asn	Pro	Pro	His	Ser	Ala	Pro	Cys	Val	Pro	Asn	
			490					495					500			
ggc	tct	gcg	ttg	ctg	ctc	tcc	aat	cca	gcc	tac	cgc	ctc	ctt	ctg	gcc	1890
Gly	Ser	Ala	Leu	Leu	Leu	Ser	Asn	Pro	Ala	Tyr	Arg	Leu	Leu	Leu	Ala	
		505					510					515				
act	tac	gcc	cgt	ccc	cct	cga	ggc	ccg	ggc	ccc	ccc	aca	ccc	gcc	tgg	1938
Thr	Tyr	Ala	Arg	Pro	Pro	Arg	Gly	Pro	Gly	Pro	Pro	Thr	Pro	Ala	Trp	
	520					525					530					
gcc	aaa	ccc	acc	aac	acc	cag	gcc	tac	agt	ggg	gac	tat	atg	gag	cct	1986
Ala	Lys	Pro	Thr	Asn	Thr	Gln	Ala	Tyr	Ser	Gly	Asp	Tyr	Met	Glu	Pro	
535					540					545					550	
gag	aag	cca	ggc	gcc	ccg	ctt	ctg	ccc	cca	cct	ccc	cag	aac	agc	gtc	2034
Glu	Lys	Pro	Gly	Ala	Pro	Leu	Leu	Pro	Pro	Pro	Pro	Gln	Asn	Ser	Val	
			555					560						565		
ccc	cat	tat	gcc	gag	gct	gac	att	gtt	acc	ctg	cag	ggc	gtc	acc	ggg	2082
Pro	His	Tyr	Ala	Glu	Ala	Asp	Ile	Val	Thr	Leu	Gln	Gly	Val	Thr	Gly	
			570					575					580			
ggc	aac	acc	tat	gct	gtg	cct	gca	ctg	ccc	cca	ggg	gca	gtc	ggg	gat	2130
Gly	Asn	Thr	Tyr	Ala	Val	Pro	Ala	Leu	Pro	Pro	Gly	Ala	Val	Gly	Asp	
		585					590					595				
ggg	ccc	ccc	aga	gtg	gat	ttc	cct	cga	tct	cga	ctc	cgc	ttc	aag	gag	2178
Gly	Pro	Pro	Arg	Val	Asp	Phe	Pro	Arg	Ser	Arg	Leu	Arg	Phe	Lys	Glu	
	600					605					610					
aag	ctt	ggc	gag	ggc	cag	ttt	ggg	gag	gtg	cac	ctg	tgt	gag	gtc	gac	2226

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Lys 615	Leu	Gly	Glu	Gly	Gln 620	Phe	Gly	Glu	Val	His 625	Leu	Cys	Glu	Val	Asp 630	
agc Ser	cct Pro	caa Gln	gat Asp	ctg Leu 635	gtt Val	agt Ser	ctt Leu	gat Asp	ttc Phe 640	ccc Pro	ctt Leu	aat Asn	gtg Val	cgt Arg 645	aag Lys	2274
gga Gly	cac His	cct Pro	ttg Leu 650	ctg Leu	gta Val	gct Ala	gtc Val	aag Lys 655	atc Ile	tta Leu	cgg Arg	cca Pro	gat Asp 660	gcc Ala	acc Thr	2322
aag Lys	aat Asn	gcc Ala 665	agc Ser	ttc Phe	tcc Ser	ttg Leu	ttc Phe 670	tcc Ser	agg Arg	aat Asn	gat Asp	ttc Phe 675	ctg Leu	aaa Lys	gag Glu	2370
gtg Val	aag Lys 680	atc Ile	atg Met	tcg Ser	agg Arg	ctc Leu 685	aag Lys	gac Asp	cca Pro	aac Asn	atc Ile 690	att Ile	cgg Arg	ctg Leu	ctg Leu	2418
ggc Gly 695	gtg Val	tgt Cys	gtg Val	cag Gln 700	gac Asp	gac Asp	ccc Pro	ctc Leu	tgc Cys	atg Met 705	att Ile	act Thr	gac Asp	tac Tyr	atg Met 710	2466
gag Glu	aac Asn	ggc Gly	gac Asp	ctc Leu 715	aac Asn	cag Gln	ttc Phe	ctc Leu	agt Ser 720	gcc Ala	cac His	cag Gln	ctg Leu	gag Glu 725	gac Asp	2514
aag Lys	gca Ala	gcc Ala	gag Glu 730	ggg Gly	gcc Ala	cct Pro	ggg Gly	gac Asp 735	ggg Gly	cag Gln	gct Ala	gcg Ala	cag Gln 740	ggg Gly	ccc Pro	2562
acc Thr	atc Ile	agc Ser 745	tac Tyr	cca Pro	atg Met	ctg Leu	ctg Leu 750	cat His	gtg Val	gca Ala	gcc Ala	cag Gln 755	atc Ile	gcc Ala	tcc Ser	2610
ggc Gly 760	atg Met	cgc Arg	tat Tyr	ctg Leu	gcc Ala	aca Thr 765	ctc Leu	aac Asn	ttt Phe	gta Val	cat His 770	cgg Arg	gac Asp	ctg Leu	gcc Ala	2658
acg Thr 775	cgg Arg	aac Asn	tgc Cys	cta Leu	gtt Val 780	ggg Gly	gaa Glu	aat Asn	ttc Phe 785	acc Thr	atc Ile	aaa Lys	atc Ile	gca Ala	gac Asp 790	2706
ttt Phe	ggc Gly	atg Met	agc Ser	cgg Arg 795	aac Asn	ctc Leu	tat Tyr	gct Ala	ggg Gly 800	gac Asp	tat Tyr	tac Tyr	cgt Arg	gtg Val 805	cag Gln	2754
ggc Gly	cgg Arg	gca Ala	gtg Val 810	ctg Leu	ccc Pro	atc Ile	cgc Arg	tgg Trp 815	atg Met	gcc Ala	tgg Trp	gag Glu	tgc Cys 820	atc Ile	ctc Leu	2802
atg Met	ggg Gly	aag Lys 825	ttc Phe	acg Thr	act Thr	gcg Ala	agt Ser 830	gac Asp	gtg Val	tgg Trp	gcc Ala	ttt Phe 835	ggt Gly	gtg Val	acc Thr	2850
ctg Leu	tgg Trp 840	gag Glu	gtg Val	ctg Leu	atg Met	ctc Leu 845	tgt Cys	agg Arg	gcc Ala	cag Gln	ccc Pro	ttt Phe	ggg Gly	tca Ser	gct Ala	2898
cac His 855	cga Arg	cga Arg	gca Ala	ggt Gly	cat His 860	cga Arg	gaa Glu	cgc Arg	ggg Gly	gga Gly 865	gtt Val	ctt Leu	ccg Pro	gga Gly	cca Pro 870	2946
ggg Gly	ccg Pro	gca Ala	gtg Val	tac Tyr 875	ctg Leu	tcc Ser	cgg Arg	ccg Pro	cct Pro 880	gcc Ala	tgc Cys	ccg Pro	cag Gln	ggc Gly 885	cta Leu	2994
tat	gag	ctg	atg	ctt	cgg	tgc	tgg	agc	cgg	gag	tct	gag	cag	cga	cca	3042

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Tyr Glu Leu Met Leu Arg Cys Trp Ser Arg Glu Ser Glu Gln Arg Pro  
890 895 900

ccc ttt tcc cag ctg cat cgg ttc ctg gca gag gat gca ctc aac acg 3090  
Pro Phe Ser Gln Leu His Arg Phe Leu Ala Glu Asp Ala Leu Asn Thr  
905 910 915

gtg tgaatcacac atccagctgc ccctccctca gggagcgcgc caggggaagc 3143  
Val

cagtgcact aaaacaagag gacacaatgg cacctctgcc cttccccctcc cgacagccca 3203

tcacctctaa tagaggcagt gagactgcag gtgggctggg cccacccagg gagctgatgc 3263

cccttctccc cttcctggac acactctcat gtcccccttcc tgttcttctc tcctagaagc 3323

ccccctgtcg cccacccagg tggctctgtg gatgggatcc tctccaccct cctctagcca 3383

tcccttgggg aaggggtggg agaaatatag gatagacact ggacatggcc cattggagca 3443

cctgggcccc actggacaac actgattcct ggagaggtgg ctgcgcccc agcttctctc 3503

tccctgtcac aactggacc ccactggctg agaactctggg ggtgaggagg acaagaagga 3563

gaggaaaatg tttccttgtg cctgctcctg tacttgtcct cagcttgggc ttcttctctc 3623

tccatcacct gaaacactgg acctgggggt agccccgccc cagccctcag tcacccccac 3683

ttcccacttg cagtcttgta gctagaactt ctctaagcct atacgtttct gtggagtaaa 3743

tattgggatt ggggggaaag agggagcaac ggcccatagc cttgggggtg gacatctcta 3803

gtgtagctgc cacattgatt tttctataat cacttgggggt ttgtacattt ttggggggag 3863

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taggcaggta ataataaagg ttgagttttc cacaaaaaaa aaaaaaa 3970

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<211> 919  
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<400> 28

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Ser Gly Asp Ala Asp Met Lys Gly His Phe Asp Pro Ala Lys Cys Arg  
20 25 30

Tyr Ala Leu Gly Met Gln Asp Arg Thr Ile Pro Asp Ser Asp Ile Ser  
35 40 45

Ala Ser Ser Ser Trp Ser Asp Ser Thr Ala Ala Arg His Ser Arg Leu  
50 55 60

Glu Ser Ser Asp Gly Asp Gly Ala Trp Cys Pro Ala Gly Ser Val Phe  
65 70 75 80

Pro Lys Glu Glu Glu Tyr Leu Gln Val Asp Leu Gln Arg Leu His Leu

Val Ala Leu Val Gly Thr Gln Gly Arg His Ala Gly Gly Leu Gly Lys  
100 105 110

Glu Phe Ser Arg Ser Tyr Arg Leu Arg Tyr Ser Arg Asp Gly Arg Arg  
115 120 125

Trp Met Gly Trp Lys Asp Arg Trp Gly Gln Glu Val Ile Ser Gly Asn  
130 135 140

Glu Asp Pro Glu Gly Val Val Leu Lys Asp Leu Gly Pro Pro Met Val  
145 150 155 160

Ala Arg Leu Val Arg Phe Tyr Pro Arg Ala Asp Arg Val Met Ser Val  
165 170 175

Cys Leu Arg Val Glu Leu Tyr Gly Cys Leu Trp Arg Asp Gly Leu Leu  
180 185 190

Ser Tyr Thr Ala Pro Val Gly Gln Thr Met Tyr Leu Ser Glu Ala Val  
195 200 205

Tyr Leu Asn Asp Ser Thr Tyr Asp Gly His Thr Val Gly Gly Leu Gln  
210 215 220

Tyr Gly Gly Leu Gly Gln Leu Ala Asp Gly Val Val Gly Leu Asp Asp  
225 230 235 240

Phe Arg Lys Ser Gln Glu Leu Arg Val Trp Pro Gly Tyr Asp Tyr Val  
245 250 255

Gly Trp Ser Asn His Ser Phe Ser Ser Gly Tyr Val Glu Met Glu Phe  
260 265 270

Glu Phe Asp Arg Leu Arg Ala Phe Gln Ala Met Gln Val His Cys Asn  
275 280 285

Asn Met His Thr Leu Gly Ala Arg Leu Pro Gly Gly Val Glu Cys Arg  
290 295 300

Phe Arg Arg Gly Pro Ala Met Ala Trp Glu Gly Glu Pro Met Arg His  
305 310 315 320

Asn Leu Gly Gly Asn Leu Gly Asp Pro Arg Ala Arg Ala Val Ser Val  
325 330 335

Pro Leu Gly Gly Arg Val Ala Arg Phe Leu Gln Cys Arg Phe Leu Phe  
340 345 350

Ala Gly Pro Trp Leu Leu Phe Ser Glu Ile Ser Phe Ile Ser Asp Val

Val Asn Asn Ser Ser Pro Ala Leu Gly Gly Thr Phe Pro Pro Ala Pro  
370 375 380

Trp Trp Pro Pro Gly Pro Pro Pro Thr Asn Phe Ser Ser Leu Glu Leu  
385 390 395 400

Glu Pro Arg Gly Gln Gln Pro Val Ala Lys Ala Glu Gly Ser Pro Thr  
405 410 415

Ala Ile Leu Ile Gly Cys Leu Val Ala Ile Ile Leu Leu Leu Leu Leu  
420 425 430

Ile Ile Ala Leu Met Leu Trp Arg Leu His Trp Arg Arg Leu Leu Ser  
435 440 445

Lys Ala Glu Arg Arg Val Leu Glu Glu Glu Leu Thr Val His Leu Ser  
450 455 460

Val Pro Gly Asp Thr Ile Leu Ile Asn Asn Arg Pro Gly Pro Arg Glu  
465 470 475 480

Pro Pro Pro Tyr Gln Glu Pro Arg Pro Arg Gly Asn Pro Pro His Ser  
485 490 495

Ala Pro Cys Val Pro Asn Gly Ser Ala Leu Leu Leu Ser Asn Pro Ala  
500 505 510

Tyr Arg Leu Leu Leu Ala Thr Tyr Ala Arg Pro Pro Arg Gly Pro Gly  
515 520 525

Pro Pro Thr Pro Ala Trp Ala Lys Pro Thr Asn Thr Gln Ala Tyr Ser  
530 535 540

Gly Asp Tyr Met Glu Pro Glu Lys Pro Gly Ala Pro Leu Leu Pro Pro  
545 550 555 560

Pro Pro Gln Asn Ser Val Pro His Tyr Ala Glu Ala Asp Ile Val Thr  
565 570 575

Leu Gln Gly Val Thr Gly Gly Asn Thr Tyr Ala Val Pro Ala Leu Pro  
580 585 590

Pro Gly Ala Val Gly Asp Gly Pro Pro Arg Val Asp Phe Pro Arg Ser  
595 600 605

Arg Leu Arg Phe Lys Glu Lys Leu Gly Glu Gly Gln Phe Gly Glu Val  
610 615 620

His Leu Cys Glu Val Asp Ser Pro Gln Asp Leu Val Ser Leu Asp Phe

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625 630 635 640

Pro Leu Asn Val Arg Lys Gly His Pro Leu Leu Val Ala Val Lys Ile  
645 650 655

Leu Arg Pro Asp Ala Thr Lys Asn Ala Ser Phe Ser Leu Phe Ser Arg  
660 665 670

Asn Asp Phe Leu Lys Glu Val Lys Ile Met Ser Arg Leu Lys Asp Pro  
675 680 685

Asn Ile Ile Arg Leu Leu Gly Val Cys Val Gln Asp Asp Pro Leu Cys  
690 695 700

Met Ile Thr Asp Tyr Met Glu Asn Gly Asp Leu Asn Gln Phe Leu Ser  
705 710 715 720

Ala His Gln Leu Glu Asp Lys Ala Ala Glu Gly Ala Pro Gly Asp Gly  
725 730 735

Gln Ala Ala Gln Gly Pro Thr Ile Ser Tyr Pro Met Leu Leu His Val  
740 745 750

Ala Ala Gln Ile Ala Ser Gly Met Arg Tyr Leu Ala Thr Leu Asn Phe  
755 760 765

Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Glu Asn Phe  
770 775 780

Thr Ile Lys Ile Ala Asp Phe Gly Met Ser Arg Asn Leu Tyr Ala Gly  
785 790 795 800

Asp Tyr Tyr Arg Val Gln Gly Arg Ala Val Leu Pro Ile Arg Trp Met  
805 810 815

Ala Trp Glu Cys Ile Leu Met Gly Lys Phe Thr Thr Ala Ser Asp Val  
820 825 830

Trp Ala Phe Gly Val Thr Leu Trp Glu Val Leu Met Leu Cys Arg Ala  
835 840 845

Gln Pro Phe Gly Ser Ala His Arg Arg Ala Gly His Arg Glu Arg Gly  
850 855 860

Gly Val Leu Pro Gly Pro Gly Pro Ala Val Tyr Leu Ser Arg Pro Pro  
865 870 875 880

Ala Cys Pro Gln Gly Leu Tyr Glu Leu Met Leu Arg Cys Trp Ser Arg  
885 890 895

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Page 64



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Thr Tyr Ile Gly Ser Val Glu Leu Val Thr Gln Gln Met Trp Val Tyr  
50 55 60

Asp Glu Asp Val Gly Ile Asn Tyr Arg Glu Val Thr Phe Val Pro Gly  
65 70 75 80

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Leu	Tyr	Lys	Ile	Phe	Asp	Glu	Ile	Leu	Val	Asn	Ala	Ala	Asp	Asn	Lys	85	90	95
Gln	Arg	Asp	Pro	Lys	Met	Ser	Cys	Ile	Arg	Val	Thr	Ile	Asp	Pro	Glu	100	105	110
Asn	Asn	Leu	Ile	Ser	Ile	Trp	Asn	Asn	Gly	Lys	Gly	Ile	Pro	Val	Val	115	120	125
Glu	His	Lys	Val	Glu	Lys	Met	Tyr	Val	Pro	Ala	Leu	Ile	Phe	Gly	Gln	130	135	140
Leu	Leu	Thr	Ser	Ser	Asn	Tyr	Asp	Asp	Asp	Glu	Lys	Lys	Val	Thr	Gly	145	150	155
Gly	Arg	Asn	Gly	Tyr	Gly	Ala	Lys	Leu	Cys	Asn	Ile	Phe	Ser	Thr	Lys	165	170	175
Phe	Thr	Val	Glu	Thr	Ala	Ser	Arg	Glu	Tyr	Lys	Lys	Met	Phe	Lys	Gln	180	185	190
Thr	Trp	Met	Asp	Asn	Met	Gly	Arg	Ala	Gly	Glu	Met	Glu	Leu	Lys	Pro	195	200	205
Phe	Asn	Gly	Glu	Asp	Tyr	Thr	Cys	Ile	Thr	Phe	Gln	Pro	Asp	Leu	Ser	210	215	220
Lys	Phe	Lys	Met	Gln	Ser	Leu	Asp	Lys	Asp	Ile	Val	Ala	Leu	Met	Val	225	230	235
Arg	Arg	Ala	Tyr	Asp	Ile	Ala	Gly	Ser	Thr	Lys	Asp	Val	Lys	Val	Phe	245	250	255
Leu	Asn	Gly	Asn	Lys	Leu	Pro	Val	Lys	Gly	Phe	Arg	Ser	Tyr	Val	Asp	260	265	270
Met	Tyr	Leu	Lys	Asp	Lys	Leu	Asp	Glu	Thr	Gly	Asn	Ser	Leu	Lys	Val	275	280	285
Ile	His	Glu	Gln	Val	Asn	His	Arg	Trp	Glu	Val	Cys	Leu	Thr	Met	Ser	290	295	300
Glu	Lys	Gly	Phe	Gln	Gln	Ile	Ser	Phe	Val	Asn	Ser	Ile	Ala	Thr	Ser	305	310	315
Lys	Gly	Gly	Arg	His	Val	Asp	Tyr	Val	Ala	Asp	Gln	Ile	Val	Thr	Lys	325	330	335
Leu	Val	Asp	Val	Val	Lys	Lys	Lys	Asn	Lys	Gly	Gly	Val	Ala	Val	Lys	340	345	350



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Ala His Gln Val Lys Asn His Met Trp Ile Phe Val Asn Ala Leu Ile  
355 360 365

Glu Asn Pro Thr Phe Asp Ser Gln Thr Lys Glu Asn Met Thr Leu Gln  
370 375 380

Pro Lys Ser Phe Gly Ser Thr Cys Gln Leu Ser Glu Lys Phe Ile Lys  
385 390 395 400

Ala Ala Ile Gly Cys Gly Ile Val Glu Ser Ile Leu Asn Trp Val Lys  
405 410 415

Phe Lys Ala Gln Val Gln Leu Asn Lys Lys Cys Ser Ala Val Lys His  
420 425 430

Asn Arg Ile Lys Gly Ile Pro Lys Leu Asp Asp Ala Asn Asp Ala Gly  
435 440 445

Gly Arg Asn Ser Thr Glu Cys Thr Leu Ile Leu Thr Glu Gly Asp Ser  
450 455 460

Ala Lys Thr Leu Ala Val Ser Gly Leu Gly Val Val Gly Arg Asp Lys  
465 470 475 480

Tyr Gly Val Phe Pro Leu Arg Gly Lys Ile Leu Asn Val Arg Glu Ala  
485 490 495

Ser His Lys Gln Ile Met Glu Asn Ala Glu Ile Asn Asn Ile Ile Lys  
500 505 510

Ile Val Gly Leu Gln Tyr Lys Lys Asn Tyr Glu Asp Glu Asp Ser Leu  
515 520 525

Lys Thr Leu Arg Tyr Gly Lys Ile Met Ile Met Thr Asp Gln Asp Gln  
530 535 540

Asp Gly Ser His Ile Lys Gly Leu Leu Ile Asn Phe Ile His His Asn  
545 550 555 560

Trp Pro Ser Leu Leu Arg His Arg Phe Leu Glu Glu Phe Ile Thr Pro  
565 570 575

Ile Val Lys Val Ser Lys Asn Lys Gln Glu Met Ala Phe Tyr Ser Leu  
580 585 590

Pro Glu Phe Glu Glu Trp Lys Ser Ser Thr Pro Asn His Lys Lys Trp  
595 600 605

Lys Val Lys Tyr Tyr Lys Gly Leu Gly Thr Ser Thr Ser Lys Glu Ala  
610 615 620

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Lys Glu Tyr Phe Ala Asp Met Lys Arg His Arg Ile Gln Phe Lys Tyr  
625 630 635 640

Ser Gly Pro Glu Asp Asp Ala Ala Ile Ser Leu Ala Phe Ser Lys Lys  
645 650 655

Gln Ile Asp Asp Arg Lys Glu Trp Leu Thr Asn Phe Met Glu Asp Arg  
660 665 670

Arg Gln Arg Lys Leu Leu Gly Leu Pro Glu Asp Tyr Leu Tyr Gly Gln  
675 680 685

Thr Thr Thr Tyr Leu Thr Tyr Asn Asp Phe Ile Asn Lys Glu Leu Ile  
690 695 700

Leu Phe Ser Asn Ser Asp Asn Glu Arg Ser Ile Pro Ser Met Val Asp  
705 710 715 720

Gly Leu Lys Pro Gly Gln Arg Lys Val Leu Phe Thr Cys Phe Lys Arg  
725 730 735

Asn Asp Lys Arg Glu Val Lys Val Ala Gln Leu Ala Gly Ser Val Ala  
740 745 750

Glu Met Ser Ser Tyr His His Gly Glu Met Ser Leu Met Met Thr Ile  
755 760 765

Ile Asn Leu Ala Gln Asn Phe Val Gly Ser Asn Asn Leu Asn Leu Leu  
770 775 780

Gln Pro Ile Gly Gln Phe Gly Thr Arg Leu His Gly Gly Lys Asp Ser  
785 790 795 800

Ala Ser Pro Arg Tyr Ile Phe Thr Met Leu Ser Ser Leu Ala Arg Leu  
805 810 815

Leu Phe Pro Pro Lys Asp Asp His Thr Leu Lys Phe Leu Tyr Asp Asp  
820 825 830

Asn Gln Arg Val Glu Pro Glu Trp Tyr Ile Pro Ile Ile Pro Met Val  
835 840 845

Leu Ile Asn Gly Ala Glu Gly Ile Gly Thr Gly Trp Ser Cys Lys Ile  
850 855 860

Pro Asn Phe Asp Val Arg Glu Ile Val Asn Asn Ile Arg Arg Leu Met  
865 870 875 880

Asp Gly Glu Glu Pro Leu Pro Met Leu Pro Ser Tyr Lys Asn Phe Lys  
885 890 895

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Gly Thr Ile Glu Glu Leu Ala Pro Asn Gln Tyr Val Ile Ser Gly Glu  
900 905 910

Val Ala Ile Leu Asn Ser Thr Thr Ile Glu Ile Ser Glu Leu Pro Val  
915 920 925

Arg Thr Trp Thr Gln Thr Tyr Lys Glu Gln Val Leu Glu Pro Met Leu  
930 935 940

Asn Gly Thr Glu Lys Thr Pro Pro Leu Ile Thr Asp Tyr Arg Glu Tyr  
945 950 955 960

His Thr Asp Thr Thr Val Lys Phe Val Val Lys Met Thr Glu Glu Lys  
965 970 975

Leu Ala Glu Ala Glu Arg Val Gly Leu His Lys Val Phe Lys Leu Gln  
980 985 990

Thr Ser Leu Thr Cys Asn Ser Met Val Leu Phe Asp His Val Gly Cys  
995 1000 1005

Leu Lys Lys Tyr Asp Thr Val Leu Asp Ile Leu Arg Asp Phe Phe  
1010 1015 1020

Glu Leu Arg Leu Lys Tyr Tyr Gly Leu Arg Lys Glu Trp Leu Leu  
1025 1030 1035

Gly Met Leu Gly Ala Glu Ser Ala Lys Leu Asn Asn Gln Ala Arg  
1040 1045 1050

Phe Ile Leu Glu Lys Ile Asp Gly Lys Ile Ile Ile Glu Asn Lys  
1055 1060 1065

Pro Lys Lys Glu Leu Ile Lys Val Leu Ile Gln Arg Gly Tyr Asp  
1070 1075 1080

Ser Asp Pro Val Lys Ala Trp Lys Glu Ala Gln Gln Lys Val Pro  
1085 1090 1095

Asp Glu Glu Glu Asn Glu Glu Ser Asp Asn Glu Lys Glu Thr Glu  
1100 1105 1110

Lys Ser Asp Ser Val Thr Asp Ser Gly Pro Thr Phe Asn Tyr Leu  
1115 1120 1125

Leu Asp Met Pro Leu Trp Tyr Leu Thr Lys Glu Lys Lys Asp Glu  
1130 1135 1140

Leu Cys Arg Leu Arg Asn Glu Lys Glu Gln Glu Leu Asp Thr Leu  
1145 1150 1155

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Lys	Arg	Lys	Ser	Pro	Ser	Asp	Leu	Trp	Lys	Glu	Asp	Leu	Ala	Thr
1160						1165					1170			
Phe	Ile	Glu	Glu	Leu	Glu	Ala	Val	Glu	Ala	Lys	Glu	Lys	Gln	Asp
1175						1180					1185			
Glu	Gln	Val	Gly	Leu	Pro	Gly	Lys	Gly	Gly	Lys	Ala	Lys	Gly	Lys
1190						1195					1200			
Lys	Thr	Gln	Met	Ala	Glu	Val	Leu	Pro	Ser	Pro	Arg	Gly	Gln	Arg
1205						1210					1215			
Val	Ile	Pro	Arg	Ile	Thr	Ile	Glu	Met	Lys	Ala	Glu	Ala	Glu	Lys
1220						1225					1230			
Lys	Asn	Lys	Lys	Lys	Ile	Lys	Asn	Glu	Asn	Thr	Glu	Gly	Ser	Pro
1235						1240					1245			
Gln	Glu	Asp	Gly	Val	Glu	Leu	Glu	Gly	Leu	Lys	Gln	Arg	Leu	Glu
1250						1255					1260			
Lys	Lys	Gln	Lys	Arg	Glu	Pro	Gly	Thr	Lys	Thr	Lys	Lys	Gln	Thr
1265						1270					1275			
Thr	Leu	Ala	Phe	Lys	Pro	Ile	Lys	Lys	Gly	Lys	Lys	Arg	Asn	Pro
1280						1285					1290			
Trp	Ser	Asp	Ser	Glu	Ser	Asp	Arg	Ser	Ser	Asp	Glu	Ser	Asn	Phe
1295						1300					1305			
Asp	Val	Pro	Pro	Arg	Glu	Thr	Glu	Pro	Arg	Arg	Ala	Ala	Thr	Lys
1310						1315					1320			
Thr	Lys	Phe	Thr	Met	Asp	Leu	Asp	Ser	Asp	Glu	Asp	Phe	Ser	Asp
1325						1330					1335			
Phe	Asp	Glu	Lys	Thr	Asp	Asp	Glu	Asp	Phe	Val	Pro	Ser	Asp	Ala
1340						1345					1350			
Ser	Pro	Pro	Lys	Thr	Lys	Thr	Ser	Pro	Lys	Leu	Ser	Asn	Lys	Glu
1355						1360					1365			
Leu	Lys	Pro	Gln	Lys	Ser	Val	Val	Ser	Asp	Leu	Glu	Ala	Asp	Asp
1370						1375					1380			
Val	Lys	Gly	Ser	Val	Pro	Leu	Ser	Ser	Ser	Pro	Pro	Ala	Thr	His
1385						1390					1395			
Phe	Pro	Asp	Glu	Thr	Glu	Ile	Thr	Asn	Pro	Val	Pro	Lys	Lys	Asn
1400						1405					1410			

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 Val Thr Val Lys Lys Thr Ala Ala Lys Ser Gln Ser Ser Thr Ser  
 1415 1420 1425

Thr Thr Gly Ala Lys Lys Arg Ala Ala Pro Lys Gly Thr Lys Arg  
 1430 1435 1440

Asp Pro Ala Leu Asn Ser Gly Val Ser Gln Lys Pro Asp Pro Ala  
 1445 1450 1455

Lys Thr Lys Asn Arg Arg Lys Arg Lys Pro Ser Thr Ser Asp Asp  
 1460 1465 1470

Ser Asp Ser Asn Phe Glu Lys Ile Val Ser Lys Ala Val Thr Ser  
 1475 1480 1485

Lys Lys Ser Lys Gly Glu Ser Asp Asp Phe His Met Asp Phe Asp  
 1490 1495 1500

Ser Ala Val Ala Pro Arg Ala Lys Ser Val Arg Ala Lys Lys Pro  
 1505 1510 1515

Ile Lys Tyr Leu Glu Glu Ser Asp Glu Asp Asp Leu Phe  
 1520 1525 1530

<210> 31  
 <211> 1369  
 <212> DNA  
 <213> homo sapiens

<220>  
 <221> CDS  
 <222> (237)..(761)

<400> 31  
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 gggacccggg cgccccgccc tcgccagcgc ccgccccgc ccgccccgg cccgccctct 180  
 gtatctggcc cctgggcagc tgcccgggga ggcggccagc gagctggggc cgcgca atg 239  
 Met  
 1  
 tcg cac gga gcc ggg ctc gtc cgc acc acg tgc agc agc ggc agc gcg 287  
 Ser His Gly Ala Gly Leu Val Arg Thr Thr Cys Ser Ser Gly Ser Ala  
 5 10 15  
 ctc gga ccc ggg gcc ggc gcg gcc cag ccc agc gcg agc ccc ttg gag 335  
 Leu Gly Pro Gly Ala Gly Ala Ala Gln Pro Ser Ala Ser Pro Leu Glu  
 20 25 30  
 ggg ctg ctg gac ctc agc tac ccc cgc acc cac gcg gcc ctg ctg aaa 383  
 Gly Leu Leu Asp Leu Ser Tyr Pro Arg Thr His Ala Ala Leu Leu Lys  
 35 40 45  
 gtg gcg caa atg gtc acc ctg ctg att gcc ttc atc tgt gtg cgg agc 431  
 Val Ala Gln Met Val Thr Leu Leu Ile Ala Phe Ile Cys Val Arg Ser  
 50 55 60 65

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tcc ctg tgg acc aac tac agc gcc tac agc tac ttt gaa gtg gtc acc	479
Ser Leu Trp Thr Asn Tyr Ser Ala Tyr Ser Tyr Phe Glu Val Val Thr	
70 75 80	
att tgc gac ttg ata atg atc ctc gcc ttt tac ctg gtc cac ctc ttc	527
Ile Cys Asp Leu Ile Met Ile Leu Ala Phe Tyr Leu Val His Leu Phe	
85 90 95	
cgc ttc tac cgc gtg ctc acc tgt atc agc tgg ccc ctg tcg gaa ctt	575
Arg Phe Tyr Arg Val Leu Thr Cys Ile Ser Trp Pro Leu Ser Glu Leu	
100 105 110	
ctg cac tat tta atc ggt acc ctg ctc ctc ctc atc gcc tcc att gtg	623
Leu His Tyr Leu Ile Gly Thr Leu Leu Leu Leu Ile Ala Ser Ile Val	
115 120 125	
gca gct tcc aag agt tac aac cag agc gga ctg gta gcc gga gcg atc	671
Ala Ala Ser Lys Ser Tyr Asn Gln Ser Gly Leu Val Ala Gly Ala Ile	
130 135 140 145	
ttt ggt ttc atg gcc acc ttc ctc tgc atg gca agc ata tgg ctg tcc	719
Phe Gly Phe Met Ala Thr Phe Leu Cys Met Ala Ser Ile Trp Leu Ser	
150 155 160	
tat aag atc tcg tgt gta acc cag tcc aca gat gca gcc gtc	761
Tyr Lys Ile Ser Cys Val Thr Gln Ser Thr Asp Ala Ala Val	
165 170 175	
tgatgaggcc acaacccta ggcccctcag gagctttgca gagaggagga cgtgtactcc	821
aggcgaggcc tctggacctg tgttcctgtg ccaaagtcct gtcaggctgg tgggcaccag	881
gaaaggcctg caccctcttc ctgctctccc aggaagccag ctccctgagc tcctgagcca	941
gccggaaact cttcctccag ctttccgggg agaacatccc tcccattctg ggaaaggaaa	1001
gcagcctcca gggaaatgtt ttctgccttc ctgcttctag aaccacctca ggtactgatg	1061
aacccccactt agcacagctg aagggggttg tgaatactcc cgcctaaatc ctttctactt	1121
cactcctcag gggagtgaag tgccttaaga aacaaagccc tgtcctaatt tatctagctt	1181
gtcagtcggtg tcttagagat accctctttc ctgaagttag gcgtgcctgt agaaacacta	1241
tgtggtcagc ctgtcccaa ggagatcttg tgtctctctt ccatctctgc ctttgttacc	1301
agtgtgcatg tgtttgtgtg ttttttaata aaatattgac tcggccagtt aaaaaaaaaa	1361
aaaaaaaa	1369

<210> 32  
 <211> 175  
 <212> PRT  
 <213> homo sapiens

<400> 32

Met Ser His Gly Ala Gly Leu Val Arg Thr Thr Cys Ser Ser Gly Ser  
 1 5 10 15

Ala Leu Gly Pro Gly Ala Gly Ala Ala Gln Pro Ser Ala Ser Pro Leu  
 20 25 30

Glu Gly Leu Leu Asp Leu Ser Tyr Pro Arg Thr His Ala Ala Leu Leu

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35

40

45

Lys Val Ala Gln Met Val Thr Leu Leu Ile Ala Phe Ile Cys Val Arg  
50 55 60

Ser Ser Leu Trp Thr Asn Tyr Ser Ala Tyr Ser Tyr Phe Glu Val Val  
65 70 75 80

Thr Ile Cys Asp Leu Ile Met Ile Leu Ala Phe Tyr Leu Val His Leu  
85 90 95

Phe Arg Phe Tyr Arg Val Leu Thr Cys Ile Ser Trp Pro Leu Ser Glu  
100 105 110

Leu Leu His Tyr Leu Ile Gly Thr Leu Leu Leu Ile Ala Ser Ile  
115 120 125

Val Ala Ala Ser Lys Ser Tyr Asn Gln Ser Gly Leu Val Ala Gly Ala  
130 135 140

Ile Phe Gly Phe Met Ala Thr Phe Leu Cys Met Ala Ser Ile Trp Leu  
145 150 155 160

Ser Tyr Lys Ile Ser Cys Val Thr Gln Ser Thr Asp Ala Ala Val  
165 170 175

<210> 33  
<211> 3470  
<212> DNA  
<213> homo sapiens

<220>  
<221> CDS  
<222> (458)..(2698)

<400> 33  
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ggagtttgga acggctgaag ttcaccttcc agcccctagc gccgttcgcg ccgctaggcc 120  
tggcttctga ggcggttgcg gtgctcggtc gccgcctagg cggggcaggg tgcgagcagg 180  
ggcttcgggc cacgcttctc ttggcgacag gattttgctg tgaagtccgt ccgggaaacg 240  
gaggaaaaaa agagttgcgg gaggtgtcg gctaataacg gttcttgata catatttgcc 300  
agacttcaag atttcagaaa aggggtgaaa gagaagattg caactttgag tcagacctgt 360  
aggcctgata gactgattaa accacagaag gtgacctgct gagaaaagtg gtacaaatac 420  
tgggaaaaaac ctgctcttct gcgttaagtg ggagaca atg tca caa gtt aaa agc 475  
Met Ser Gln Val Lys Ser  
1 5  
tct tat tcc tat gat gcc ccc tcg gat ttc atc aat ttt tca tcc ttg 523  
Ser Tyr Ser Tyr Asp Ala Pro Ser Asp Phe Ile Asn Phe Ser Ser Leu  
10 15 20

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gat	gat	gaa	gga	gat	act	caa	aac	ata	gat	tca	tgg	ttt	gag	gag	aag	571
Asp	Asp	Glu	Gly	Asp	Thr	Gln	Asn	Ile	Asp	Ser	Trp	Phe	Glu	Glu	Lys	
		25					30					35				
gcc	aat	ttg	gag	aat	aag	tta	ctg	ggg	aag	aat	gga	act	gga	ggg	ctt	619
Ala	Asn	Leu	Glu	Asn	Lys	Leu	Leu	Gly	Lys	Asn	Gly	Thr	Gly	Gly	Leu	
	40					45					50					
ttt	cag	ggc	aaa	act	cct	ttg	aga	aag	gct	aat	ctt	cag	caa	gct	att	667
Phe	Gln	Gly	Lys	Thr	Pro	Leu	Arg	Lys	Ala	Asn	Leu	Gln	Gln	Ala	Ile	
55					60					65					70	
gtc	aca	cct	ttg	aaa	cca	gtt	gac	aac	act	tac	tac	aaa	gag	gca	gaa	715
Val	Thr	Pro	Leu	Lys	Pro	Val	Asp	Asn	Thr	Tyr	Tyr	Lys	Glu	Ala	Glu	
				75					80					85		
aaa	gaa	aat	ctt	gtg	gaa	caa	tcc	att	ccg	tca	aat	gct	tgt	tct	tcc	763
Lys	Glu	Asn	Leu	Val	Glu	Gln	Ser	Ile	Pro	Ser	Asn	Ala	Cys	Ser	Ser	
			90					95					100			
ctg	gaa	gtt	gag	gca	gcc	ata	tca	aga	aaa	act	cca	gcc	cag	cct	cag	811
Leu	Glu	Val	Glu	Ala	Ala	Ile	Ser	Arg	Lys	Thr	Pro	Ala	Gln	Pro	Gln	
		105					110					115				
aga	aga	tct	ctt	agg	ctt	tct	gct	cag	aag	gat	ttg	gaa	cag	aaa	gaa	859
Arg	Arg	Ser	Leu	Arg	Leu	Ser	Ala	Gln	Lys	Asp	Leu	Glu	Gln	Lys	Glu	
	120					125					130					
aag	cat	cat	gta	aaa	atg	aaa	gcc	aag	aga	tgt	gcc	act	cct	gta	atc	907
Lys	His	His	Val	Lys	Met	Lys	Ala	Lys	Arg	Cys	Ala	Thr	Pro	Val	Ile	
135					140					145					150	
atc	gat	gaa	att	cta	ccc	tct	aag	aaa	atg	aaa	gtt	tct	aac	aac	aaa	955
Ile	Asp	Glu	Ile	Leu	Pro	Ser	Lys	Lys	Met	Lys	Val	Ser	Asn	Asn	Lys	
				155					160					165		
aag	aag	cca	gag	gaa	gaa	ggc	agt	gct	cat	caa	gat	act	gct	gaa	aag	1003
Lys	Lys	Pro	Glu	Glu	Glu	Gly	Ser	Ala	His	Gln	Asp	Thr	Ala	Glu	Lys	
			170					175					180			
aat	gca	tct	tcc	cca	gag	aaa	gcc	aag	ggt	aga	cat	act	gtg	cct	tgt	1051
Asn	Ala	Ser	Ser	Pro	Glu	Lys	Ala	Lys	Gly	Arg	His	Thr	Val	Pro	Cys	
		185					190					195				
atg	cca	cct	gca	aag	cag	aag	ttt	cta	aaa	agt	act	gag	gag	caa	gag	1099
Met	Pro	Pro	Ala	Lys	Gln	Lys	Phe	Leu	Lys	Ser	Thr	Glu	Glu	Gln	Glu	
	200					205					210					
ctg	gag	aag	agt	atg	aaa	atg	cag	caa	gag	gtg	gtg	gag	atg	cgg	aaa	1147
Leu	Glu	Lys	Ser	Met	Lys	Met	Gln	Gln	Glu	Val	Val	Glu	Met	Arg	Lys	
215					220					225					230	
aag	aat	gaa	gaa	ttc	aag	aaa	ctt	gct	ctg	gct	gga	ata	ggg	caa	cct	1195
Lys	Asn	Glu	Glu	Phe	Lys	Lys	Leu	Ala	Leu	Ala	Gly	Ile	Gly	Gln	Pro	
				235					240					245		
gtg	aag	aaa	tca	gtg	agc	cag	gtc	acc	aaa	tca	gtt	gac	ttc	cac	ttc	1243
Val	Lys	Lys	Ser	Val	Ser	Gln	Val	Thr	Lys	Ser	Val	Asp	Phe	His	Phe	
			250					255					260			
cgc	aca	gat	gag	cga	atc	aaa	caa	cat	cct	aag	aac	cag	gag	gaa	tat	1291
Arg	Thr	Asp	Glu	Arg	Ile	Lys	Gln	His	Pro	Lys	Asn	Gln	Glu	Glu	Tyr	
		265					270					275				
aag	gaa	gtg	aac	ttt	aca	tct	gaa	cta	cga	aag	cat	cct	tca	tct	cct	1339
Lys	Glu	Val	Asn	Phe	Thr	Ser	Glu	Leu	Arg	Lys	His	Pro	Ser	Ser	Pro	
	280					285					290					



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gcc cga gtg act aag gga tgt acc att gtt aag cct ttc aac ctg tcc Ala Arg Val Thr Lys Gly Cys Thr Ile Val Lys Pro Phe Asn Leu Ser 295 300 305 310	1387
caa gga aag aaa aga aca ttt gat gaa aca gtt tct aca tat gtg ccc Gln Gly Lys Lys Arg Thr Phe Asp Glu Thr Val Ser Thr Tyr Val Pro 315 320 325	1435
ctt gca cag caa gtt gaa gac ttc cat aaa cga acc cct aac aga tat Leu Ala Gln Gln Val Glu Asp Phe His Lys Arg Thr Pro Asn Arg Tyr 330 335 340	1483
cat ttg agg agc aag aag gat gat att aac ctg tta ccc tcc aaa tct His Leu Arg Ser Lys Lys Asp Asp Ile Asn Leu Leu Pro Ser Lys Ser 345 350 355	1531
tct gtg acc aag att tgc aga gac cca cag act cct gta ctg caa acc Ser Val Thr Lys Ile Cys Arg Asp Pro Gln Thr Pro Val Leu Gln Thr 360 365 370	1579
aaa cac cgt gca cgg gct gtg acc tgc aaa agt aca gca gag ctg gag Lys His Arg Ala Arg Ala Val Thr Cys Lys Ser Thr Ala Glu Leu Glu 375 380 385 390	1627
gct gag gag ctc gag aaa ttg caa caa tac aaa ttc aaa gca cgt gaa Ala Glu Glu Leu Glu Lys Leu Gln Gln Tyr Lys Phe Lys Ala Arg Glu 395 400 405	1675
ctt gat ccc aga ata ctt gaa ggt ggg ccc atc ttg ccc aag aaa cca Leu Asp Pro Arg Ile Leu Glu Gly Gly Pro Ile Leu Pro Lys Lys Pro 410 415 420	1723
cct gtg aaa cca ccc acc gag cct att ggc ttt gat ttg gaa att gag Pro Val Lys Pro Pro Thr Glu Pro Ile Gly Phe Asp Leu Glu Ile Glu 425 430 435	1771
aaa aga atc cag gag cga gaa tca aag aag aaa aca gag gat gaa cac Lys Arg Ile Gln Glu Arg Glu Ser Lys Lys Lys Thr Glu Asp Glu His 440 445 450	1819
ttt gaa ttt cat tcc aga cct tgc cct act aag att ttg gaa gat gtt Phe Glu Phe His Ser Arg Pro Cys Pro Thr Lys Ile Leu Glu Asp Val 455 460 465 470	1867
gtg ggt gtt cct gaa aag aag gta ctt cca atc acc gtc ccc aag tca Val Gly Val Pro Glu Lys Lys Val Leu Pro Pro Ile Thr Val Pro Lys Ser 475 480 485	1915
cca gcc ttt gca ttg aag aac aga att cga atg ccc acc aaa gaa gat Pro Ala Phe Ala Leu Lys Asn Arg Ile Arg Met Pro Thr Lys Glu Asp 490 495 500	1963
gag gaa gag gac gaa ccg gta gtg ata aaa gct caa cct gtg cca cat Glu Glu Glu Asp Glu Pro Val Val Ile Lys Ala Gln Pro Val Pro His 505 510 515	2011
tat ggg gtg cct ttt aag ccc caa atc cca gag gca aga act gtg gaa Tyr Gly Val Pro Phe Lys Pro Gln Ile Pro Glu Ala Arg Thr Val Glu 520 525 530	2059
ata tgc cct ttc tcg ttt gat tct cga gac aaa gaa cgt cag tta cag Ile Cys Pro Phe Ser Phe Asp Ser Arg Asp Lys Glu Arg Gln Leu Gln 535 540 545 550	2107
aag gag aag aaa ata aaa gaa ctg cag aaa ggg gag gtg ccc aag ttc Lys Glu Lys Lys Ile Lys Glu Leu Gln Lys Gly Glu Val Pro Lys Phe 555 560 565	2155

122257 sequence listing May 10 2006.ST25.txt

aag gca ctt ccc ttg cct cat ttt gac acc att aac ctg cca gag aag Lys Ala Leu Pro Leu Pro His Phe Asp Thr Ile Asn Leu Pro Glu Lys 570 575 580	2203
aag gta aag aat gtg acc cag att gaa cct ttc tgc ttg gag act gac Lys Val Lys Asn Val Thr Gln Ile Glu Pro Phe Cys Leu Glu Thr Asp 585 590 595	2251
aga aga ggt gct ctg aag gca cag act tgg aag cac cag ctg gaa gaa Arg Arg Gly Ala Leu Lys Ala Gln Thr Trp Lys His Gln Leu Glu Glu 600 605 610	2299
gaa ctg aga cag cag aaa gaa gca gct tgt ttc aag gct cgt cca aac Glu Leu Arg Gln Gln Lys Glu Ala Ala Cys Phe Lys Ala Arg Pro Asn 615 620 625 630	2347
acc gtc atc tct cag gag ccc ttt gtt ccc aag aaa gag aag aaa tca Thr Val Ile Ser Gln Glu Pro Phe Val Pro Lys Lys Glu Lys Lys Ser 635 640 645	2395
gtt gct gag ggc ctt tct ggt tct cta gtt cag gaa cct ttt cag ctg Val Ala Glu Gly Leu Ser Gly Ser Leu Val Gln Glu Pro Phe Gln Leu 650 655 660	2443
gct act gag aag aga gcc aaa gag cgg cag gag ctg gag aag aga atg Ala Thr Glu Lys Arg Ala Lys Glu Arg Gln Glu Leu Glu Lys Arg Met 665 670 675	2491
gct gag gta gaa gcc cag aaa gcc cag cag ttg gag gag gcc aga cta Ala Glu Val Glu Ala Gln Lys Ala Gln Gln Leu Glu Glu Ala Arg Leu 680 685 690	2539
cag gag gaa gag cag aaa aaa gag gag ctg gcc agg cta cgg aga gaa Gln Glu Glu Glu Gln Lys Lys Glu Glu Leu Ala Arg Leu Arg Arg Glu 695 700 705 710	2587
ctg gtg cat aag gca aat cca ata cgc aag tac cag ggt ctg gag ata Leu Val His Lys Ala Asn Pro Ile Arg Lys Tyr Gln Gly Leu Glu Ile 715 720 725	2635
aag tca agt gac cag cct ctg act gtg cct gta tct ccc aaa ttc tcc Lys Ser Ser Asp Gln Pro Leu Thr Val Pro Val Ser Pro Lys Phe Ser 730 735 740	2683
act cga ttc cac tgc taaactcagc tgtgagctgc ggataccgcc cggcaatggg Thr Arg Phe His Cys 745	2738
acctgctctt aacctcaaac ctaggaccgt cttgctttgt cattgggcat ggagagaacc	2798
cattttctcca gacttttacc tacccgtgcc tgagaaagca tacttgacaa ctgtggactc	2858
cagttttgtt gagaattgtt ttcttacatt actaaggcta ataatgagat gtaactcatg	2918
aatgtctcga ttagactcca tgtagttact tcctttaaac catcagccgg ccttttatat	2978
gggtcttcac tctgactaga atttagtctc tgtgtcagca cagtgtaatc tctattgcta	3038
ttgcccccta cgactctcac cctctcccca ctttttttaa aaattttaac cagaaaataa	3098
agatagttaa atcctaagat agagattaag tcatgggtta aatgaggaac aatcagtaaa	3158
tcagattctg tcctcttctc tgcataaccgt gaatttatag ttaaggatcc ctttgctgtg	3218
agggtagaaa acctcaccaa ctgcaccagt gaggaagaag actgcgtgga ttcatgggga	3278
gcctcacagc agccacgcag caggctctgg gtggggctgc cgtaaaggca cgttctttcc	3338

122257 sequence listing May 10 2006.ST25.txt  
 ttactggtgc tgataacaac agggaaccgt gcagtgtgca ttttaagacc tggcctggaa 3398  
 taaatacggtt ttgtctttcc ctcaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3458  
 aaaaaaaaaa aa 3470

<210> 34  
 <211> 747  
 <212> PRT  
 <213> homo sapiens

<400> 34

Met Ser Gln Val Lys Ser Ser Tyr Ser Tyr Asp Ala Pro Ser Asp Phe  
 1 5 10 15

Ile Asn Phe Ser Ser Leu Asp Asp Glu Gly Asp Thr Gln Asn Ile Asp  
 20 25 30

Ser Trp Phe Glu Glu Lys Ala Asn Leu Glu Asn Lys Leu Leu Gly Lys  
 35 40 45

Asn Gly Thr Gly Gly Leu Phe Gln Gly Lys Thr Pro Leu Arg Lys Ala  
 50 55 60

Asn Leu Gln Gln Ala Ile Val Thr Pro Leu Lys Pro Val Asp Asn Thr  
 65 70 75 80

Tyr Tyr Lys Glu Ala Glu Lys Glu Asn Leu Val Glu Gln Ser Ile Pro  
 85 90 95

Ser Asn Ala Cys Ser Ser Leu Glu Val Glu Ala Ala Ile Ser Arg Lys  
 100 105 110

Thr Pro Ala Gln Pro Gln Arg Arg Ser Leu Arg Leu Ser Ala Gln Lys  
 115 120 125

Asp Leu Glu Gln Lys Glu Lys His His Val Lys Met Lys Ala Lys Arg  
 130 135 140

Cys Ala Thr Pro Val Ile Ile Asp Glu Ile Leu Pro Ser Lys Lys Met  
 145 150 155 160

Lys Val Ser Asn Asn Lys Lys Lys Pro Glu Glu Glu Gly Ser Ala His  
 165 170 175

Gln Asp Thr Ala Glu Lys Asn Ala Ser Ser Pro Glu Lys Ala Lys Gly  
 180 185 190

Arg His Thr Val Pro Cys Met Pro Pro Ala Lys Gln Lys Phe Leu Lys  
 195 200 205

Ser Thr Glu Glu Gln Glu Leu Glu Lys Ser Met Lys Met Gln Gln Glu  
 210 215 220

122257 sequence listing May 10 2006.ST25.txt

Val Val Glu Met Arg Lys Lys Asn Glu Glu Phe Lys Lys Leu Ala Leu  
225 230 235 240

Ala Gly Ile Gly Gln Pro Val Lys Lys Ser Val Ser Gln Val Thr Lys  
245 250 255

Ser Val Asp Phe His Phe Arg Thr Asp Glu Arg Ile Lys Gln His Pro  
260 265 270

Lys Asn Gln Glu Glu Tyr Lys Glu Val Asn Phe Thr Ser Glu Leu Arg  
275 280 285

Lys His Pro Ser Ser Pro Ala Arg Val Thr Lys Gly Cys Thr Ile Val  
290 295 300

Lys Pro Phe Asn Leu Ser Gln Gly Lys Lys Arg Thr Phe Asp Glu Thr  
305 310 315 320

Val Ser Thr Tyr Val Pro Leu Ala Gln Gln Val Glu Asp Phe His Lys  
325 330 335

Arg Thr Pro Asn Arg Tyr His Leu Arg Ser Lys Lys Asp Asp Ile Asn  
340 345 350

Leu Leu Pro Ser Lys Ser Ser Val Thr Lys Ile Cys Arg Asp Pro Gln  
355 360 365

Thr Pro Val Leu Gln Thr Lys His Arg Ala Arg Ala Val Thr Cys Lys  
370 375 380

Ser Thr Ala Glu Leu Glu Ala Glu Glu Leu Glu Lys Leu Gln Gln Tyr  
385 390 395 400

Lys Phe Lys Ala Arg Glu Leu Asp Pro Arg Ile Leu Glu Gly Gly Pro  
405 410 415

Ile Leu Pro Lys Lys Pro Pro Val Lys Pro Pro Thr Glu Pro Ile Gly  
420 425 430

Phe Asp Leu Glu Ile Glu Lys Arg Ile Gln Glu Arg Glu Ser Lys Lys  
435 440 445

Lys Thr Glu Asp Glu His Phe Glu Phe His Ser Arg Pro Cys Pro Thr  
450 455 460

Lys Ile Leu Glu Asp Val Val Gly Val Pro Glu Lys Lys Val Leu Pro  
465 470 475 480

Ile Thr Val Pro Lys Ser Pro Ala Phe Ala Leu Lys Asn Arg Ile Arg  
485 490 495

122257 sequence listing May 10 2006.ST25.txt

Met Pro Thr Lys Glu Asp Glu Glu Glu Asp Glu Pro Val Val Ile Lys  
500 505 510

Ala Gln Pro Val Pro His Tyr Gly Val Pro Phe Lys Pro Gln Ile Pro  
515 520 525

Glu Ala Arg Thr Val Glu Ile Cys Pro Phe Ser Phe Asp Ser Arg Asp  
530 535 540

Lys Glu Arg Gln Leu Gln Lys Glu Lys Lys Ile Lys Glu Leu Gln Lys  
545 550 555 560

Gly Glu Val Pro Lys Phe Lys Ala Leu Pro Leu Pro His Phe Asp Thr  
565 570 575

Ile Asn Leu Pro Glu Lys Lys Val Lys Asn Val Thr Gln Ile Glu Pro  
580 585 590

Phe Cys Leu Glu Thr Asp Arg Arg Gly Ala Leu Lys Ala Gln Thr Trp  
595 600 605

Lys His Gln Leu Glu Glu Glu Leu Arg Gln Gln Lys Glu Ala Ala Cys  
610 615 620

Phe Lys Ala Arg Pro Asn Thr Val Ile Ser Gln Glu Pro Phe Val Pro  
625 630 635 640

Lys Lys Glu Lys Lys Ser Val Ala Glu Gly Leu Ser Gly Ser Leu Val  
645 650 655

Gln Glu Pro Phe Gln Leu Ala Thr Glu Lys Arg Ala Lys Glu Arg Gln  
660 665 670

Glu Leu Glu Lys Arg Met Ala Glu Val Glu Ala Gln Lys Ala Gln Gln  
675 680 685

Leu Glu Glu Ala Arg Leu Gln Glu Glu Glu Gln Lys Lys Glu Glu Leu  
690 695 700

Ala Arg Leu Arg Arg Glu Leu Val His Lys Ala Asn Pro Ile Arg Lys  
705 710 715 720

Tyr Gln Gly Leu Glu Ile Lys Ser Ser Asp Gln Pro Leu Thr Val Pro  
725 730 735

Val Ser Pro Lys Phe Ser Thr Arg Phe His Cys  
740 745

<210> 35  
<211> 1246

## 122257 sequence listing May 10 2006.ST25.txt

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (112)..(795)

&lt;400&gt; 35

gaccagccta cagccgcctg catctgtatc cagcgccagg tcccgccagt cccagctgcg 60

cgcgcccccc agtcccgcac ccgttcggcc caggctaagt tagccctcac c atg ccg 117  
Met Pro  
1gtc aaa gga ggc acc aag tgc atc aaa tac ctg ctg ttc gga ttt aac 165  
Val Lys Gly Gly Thr Lys Cys Ile Lys Tyr Leu Leu Phe Gly Phe Asn  
5 10 15ttc atc ttc tgg ctt gcc ggg att gct gtc ctt gcc att gga cta tgg 213  
Phe Ile Phe Trp Leu Ala Gly Ile Ala Val Leu Ala Ile Gly Leu Trp  
20 25 30ctc cga ttc gac tct cag acc aag agc atc ttc gag caa gaa act aat 261  
Leu Arg Phe Asp Ser Gln Thr Lys Ser Ile Phe Glu Gln Glu Thr Asn  
35 40 45 50aat aat aat tcc agc ttc tac aca gga gtc tat att ctg atc gga gcc 309  
Asn Asn Asn Ser Ser Phe Tyr Thr Gly Val Tyr Ile Leu Ile Gly Ala  
55 60 65ggc gcc ctc atg atg ctg gtg ggc ttc ctg ggc tgc tgc ggg gct gtg 357  
Gly Ala Leu Met Met Leu Val Gly Phe Leu Gly Cys Cys Gly Ala Val  
70 75 80cag gag tcc cag tgc atg ctg gga ctg ttc ttc ggc ttc ctc ttg gtg 405  
Gln Glu Ser Gln Cys Met Leu Gly Leu Phe Phe Gly Phe Leu Leu Val  
85 90 95ata ttc gcc att gaa ata gct gcg gcc atc tgg gga tat tcc cac aag 453  
Ile Phe Ala Ile Glu Ile Ala Ala Ile Trp Gly Tyr Ser His Lys  
100 105 110gat gag gtg att aag gaa gtc cag gag ttt tac aag gac acc tac aac 501  
Asp Glu Val Ile Lys Glu Val Gln Glu Phe Tyr Lys Asp Thr Tyr Asn  
115 120 125 130aag ctg aaa acc aag gat gag ccc cag cgg gaa acg ctg aaa gcc atc 549  
Lys Leu Lys Thr Lys Asp Glu Pro Gln Arg Glu Thr Leu Lys Ala Ile  
135 140 145cac tat gcg ttg aac tgc tgt ggt ttg gct ggg ggc gtg gaa cag ttt 597  
His Tyr Ala Leu Asn Cys Cys Gly Leu Ala Gly Gly Val Glu Gln Phe  
150 155 160atc tca gac atc tgc ccc aag aag gac gta ctc gaa acc ttc acc gtg 645  
Ile Ser Asp Ile Cys Pro Lys Lys Asp Val Leu Glu Thr Phe Thr Val  
165 170 175aag tcc tgt cct gat gcc atc aaa gag gtc ttc gac aat aaa ttc cac 693  
Lys Ser Cys Pro Asp Ala Ile Lys Glu Val Phe Asp Asn Lys Phe His  
180 185 190atc atc ggc gca gtg ggc atc ggc att gcc gtg gtc atg ata ttt ggc 741  
Ile Ile Gly Ala Val Gly Ile Gly Ile Ala Val Val Met Ile Phe Gly  
195 200 205 210

atg atc ttc agt atg atc ttg tgc tgt gct atc cgc agg aac cgc gag 789

122257 sequence listing May 10 2006.ST25.txt  
Met Ile Phe Ser Met Ile Leu Cys Cys Ala Ile Arg Arg Asn Arg Glu  
215 220 225

atg gtc tagagtcagc ttacatccct gagcaggaaa gtttacccat gaagattggt 845  
Met Val

gggatttttt gtttgtttgt tttgttttgt ttgttgtttg ttgtttgttt ttttgccact 905  
aatttttagta ttcatctcgc attgctagat aaaagctgaa gttactttat gtttgtcttt 965  
taatgcttca ttcaatattg acatttgtag ttgagcgggg ggtttggttt gctttgggtt 1025  
atattttttc agttgtttgt ttttgcttgt tatattaagc agaaatcctg caatgaaagg 1085  
tactatatctt gctagactct agacaagata ttgtacataa aagaattttt ttgtctttaa 1145  
atagatacaa atgtctatca actttaatca agttgtaact tatattgaag acaatttgat 1205  
acataataaaa aaattatgac aatgtcaaaa aaaaaaaaaa a 1246

<210> 36  
<211> 228  
<212> PRT  
<213> homo sapiens

<400> 36

Met Pro Val Lys Gly Gly Thr Lys Cys Ile Lys Tyr Leu Leu Phe Gly  
1 5 10 15

Phe Asn Phe Ile Phe Trp Leu Ala Gly Ile Ala Val Leu Ala Ile Gly  
20 25 30

Leu Trp Leu Arg Phe Asp Ser Gln Thr Lys Ser Ile Phe Glu Gln Glu  
35 40 45

Thr Asn Asn Asn Asn Ser Ser Phe Tyr Thr Gly Val Tyr Ile Leu Ile  
50 55 60

Gly Ala Gly Ala Leu Met Met Leu Val Gly Phe Leu Gly Cys Cys Gly  
65 70 75 80

Ala Val Gln Glu Ser Gln Cys Met Leu Gly Leu Phe Phe Gly Phe Leu  
85 90 95

Leu Val Ile Phe Ala Ile Glu Ile Ala Ala Ala Ile Trp Gly Tyr Ser  
100 105 110

His Lys Asp Glu Val Ile Lys Glu Val Gln Glu Phe Tyr Lys Asp Thr  
115 120 125

Tyr Asn Lys Leu Lys Thr Lys Asp Glu Pro Gln Arg Glu Thr Leu Lys  
130 135 140

Ala Ile His Tyr Ala Leu Asn Cys Cys Gly Leu Ala Gly Gly Val Glu  
145 150 155 160

122257 sequence listing May 10 2006.ST25.txt

Gln Phe Ile Ser Asp Ile Cys Pro Lys Lys Asp Val Leu Glu Thr Phe  
165 170 175

Thr Val Lys Ser Cys Pro Asp Ala Ile Lys Glu Val Phe Asp Asn Lys  
180 185 190

Phe His Ile Ile Gly Ala Val Gly Ile Gly Ile Ala Val Val Met Ile  
195 200 205

Phe Gly Met Ile Phe Ser Met Ile Leu Cys Cys Ala Ile Arg Arg Asn  
210 215 220

Arg Glu Met Val  
225

<210> 37  
<211> 7557  
<212> DNA  
<213> homo sapiens

<220>  
<221> CDS  
<222> (958)..(6942)

<400> 37  
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taacttcctt actctttctc tcaagaggag gcaagtggct gtggcggccg cagcagtggc 180  
tgatcatcac tgaaaatacc aaagaaaaga actgagctgc ctcttcata ttttttccat 240  
tgaggattaa tttaccgtgc tttttcattt tctctacatc ctgcaaaagt ttttttctct 300  
cctaagaaac aaactatgaa ctgattgttg aaaaaaagaa gtaaaaagtt ttagcacagc 360  
ttctctgtct cttcgggaca agttagaaaa ttctgaagtg agccgaagca tagtaagtgc 420  
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tccgagagga agaaagggtt gataatcaat caaaaatgag gtattccttt gagtatttgt 540  
gattttctta ctatattgta agatgctttt aattttctct gtaaaatagg cagaaatggt 600  
tttagtgtgt gtatgtgtga aataaaagct cagaaaagca atcttcagag cgccactgaa 660  
ggaagttttg acgaacggag tagagatgta taccacttgg gggcttcagt gagaaccag 720  
aattcctgga ggaggattta cattcagaaa tgttgaagtg aaaattcctt ctggttcagc 780  
atcttgaggt tcagcttgga agaacatttt acgtatggaa gaatttgctt ctccaaacct 840  
ctcttttggc cattgtgtgt cctgaaggat gggacaactt gtgctgtaga agcactgctt 900  
gcctgagttt gcttcaggca ttttaaattt aacttgaggg atcatgtgtt tggcatg 957  
atg agg acc act gaa gac ttc cac aag cct agt gcc aca tta aac tct 1005  
Met Arg Thr Thr Glu Asp Phe His Lys Pro Ser Ala Thr Leu Asn Ser  
1 5 10 15



122257 sequence listing May 10 2006.ST25.txt

aac acg gcc acc aag gga agg tac att tat ctg gag gca ttc ctg gag	1053
Asn Thr Ala Thr Lys Gly Arg Tyr Ile Tyr Leu Glu Ala Phe Leu Glu	
	20 25 30
gga gga gct ccc tgg ggt ttt act cta aag ggt ggc ctg gag cac gga	1101
Gly Gly Ala Pro Trp Gly Phe Thr Leu Lys Gly Gly Leu Glu His Gly	
	35 40 45
gaa cca tta atc atc tct aag gtc gaa gaa ggg ggc aaa gca gac acc	1149
Glu Pro Leu Ile Ile Ser Lys Val Glu Glu Gly Gly Lys Ala Asp Thr	
	50 55 60
ctg agc tcc aaa ctg cag gct ggg gat gag gtt gtg cac atc aat gag	1197
Leu Ser Ser Lys Leu Gln Ala Gly Asp Glu Val Val His Ile Asn Glu	
	65 70 75 80
gtg act ctg agc agc tcc aga aag gag gca gtt tcc ctg gtg aaa gga	1245
Val Thr Leu Ser Ser Ser Arg Lys Glu Ala Val Ser Leu Val Lys Gly	
	85 90 95
tcc tac aag acc ctc agg ctg gta gtg cgc aga gat gtg tgc aca gac	1293
Ser Tyr Lys Thr Leu Arg Leu Val Val Arg Arg Asp Val Cys Thr Asp	
	100 105 110
cca ggc cat gca gat act ggt gcc tct aac ttc gtc agc cca gaa cac	1341
Pro Gly His Ala Asp Thr Gly Ala Ser Asn Phe Val Ser Pro Glu His	
	115 120 125
ctc acc tct ggc ccc cag cac agg aaa gca gcg tgg tca gga ggg gtt	1389
Leu Thr Ser Gly Pro Gln His Arg Lys Ala Ala Trp Ser Gly Gly Val	
	130 135 140
aaa ctt cgg ctg aag cac agg tct agt gag cct gca ggc cga cct cac	1437
Lys Leu Arg Leu Lys His Arg Ser Ser Glu Pro Ala Gly Arg Pro His	
	145 150 155 160
tcg tgg cac aca act aaa tct ggg gag aag caa ccc gat gcc agc atg	1485
Ser Trp His Thr Thr Lys Ser Gly Glu Lys Gln Pro Asp Ala Ser Met	
	165 170 175
atg cag ata tct cag ggt atg atc ggc cct cct tgg cac caa agc tac	1533
Met Gln Ile Ser Gln Gly Met Ile Gly Pro Pro Trp His Gln Ser Tyr	
	180 185 190
cat tcc agc tcc tct act agt gac ctc tcc aac tat gac cat gct tat	1581
His Ser Ser Ser Thr Ser Asp Leu Ser Asn Tyr Asp His Ala Tyr	
	195 200 205
cta agg cgg agc cct gac cag tgc agc tcc cag ggg agc atg gag agc	1629
Leu Arg Arg Ser Pro Asp Gln Cys Ser Ser Gln Gly Ser Met Glu Ser	
	210 215 220
ctg gag ccc agt ggg gca tac cca ccc tgt cat ctt tcc cct gcc aag	1677
Leu Glu Pro Ser Gly Ala Tyr Pro Pro Cys His Leu Ser Pro Ala Lys	
	225 230 235 240
tcc acc ggc agc att gac cag ctc agc cac ttc cat aac aag aga gac	1725
Ser Thr Gly Ser Ile Asp Gln Leu Ser His Phe His Asn Lys Arg Asp	
	245 250 255
tcg gct tac agc tct ttc tcc acc agt tct agc atc cta gag tat cca	1773
Ser Ala Tyr Ser Ser Phe Ser Thr Ser Ser Ile Leu Glu Tyr Pro	
	260 265 270
cac cct ggc atc tct gcc cgg gag cgt tca ggc tcc atg gac aat act	1821
His Pro Gly Ile Ser Ala Arg Glu Arg Ser Gly Ser Met Asp Asn Thr	
	275 280 285

122257 sequence listing May 10 2006.ST25.txt

tct gct cga ggt ggc ctc ctc gaa ggg atg agg cag gca gat att cgc Ser Ala Arg Gly Gly Leu Leu Glu Gly Met Arg Gln Ala Asp Ile Arg 290 295 300	1869
tat gtc aag aca gtc tat gac acc cgg agg gga gtc tca gca gag tat Tyr Val Lys Thr Val Tyr Asp Thr Arg Arg Gly Val Ser Ala Glu Tyr 305 310 315 320	1917
gag gtg aac tct tca gcc ctg ctg ctt caa ggt agg gag gcc cga gcc Glu Val Asn Ser Ser Ala Leu Leu Leu Gln Gly Arg Glu Ala Arg Ala 325 330 335	1965
tca gca aat ggt cag ggc tat gat aaa tgg tct aat att cct cgg ggc Ser Ala Asn Gly Gln Gly Tyr Asp Lys Trp Ser Asn Ile Pro Arg Gly 340 345 350	2013
aag gga gtg cca ccc cca tcc tgg agc cag cag tgc ccc agt tcc ttg Lys Gly Val Pro Pro Pro Ser Trp Ser Gln Gln Cys Pro Ser Ser Leu 355 360 365	2061
gag act gcc acg gac aac ctt cct cct aag gtg ggt gca ccc ctg cct Glu Thr Ala Thr Asp Asn Leu Pro Pro Lys Val Gly Ala Pro Leu Pro 370 375 380	2109
cca gct cgg agt gac agt tac gca gca ttt cgg cac cgt gag cgg ccc Pro Ala Arg Ser Asp Ser Tyr Ala Ala Phe Arg His Arg Glu Arg Pro 385 390 400	2157
agc tcc tgg tct agc ctt gat cag aaa cgg ctc tgc cgg cct cag gca Ser Ser Trp Ser Ser Leu Asp Gln Lys Arg Leu Cys Arg Pro Gln Ala 405 410 415	2205
aac tct tta ggc tcc ctg aag tct cca ttc ata gag gag cag ctg cat Asn Ser Leu Gly Ser Leu Lys Ser Pro Phe Ile Glu Glu Gln Leu His 420 425 430	2253
act gtg ctg gag aag agt cca gag aac agc ccc cca gtg aag ccc aag Thr Val Leu Glu Lys Ser Pro Glu Asn Ser Pro Pro Val Lys Pro Lys 435 440 445	2301
cat aac tat acc cag aag gcc caa cct ggc caa cct ctg ctg ccg acc His Asn Tyr Thr Gln Lys Ala Gln Pro Gly Gln Pro Leu Leu Pro Thr 450 455 460	2349
agc atc tac gcg gta cct tcc ctg gag cca cac ttt gcc cag gtg cct Ser Ile Tyr Ala Val Pro Ser Leu Glu Pro His Phe Ala Gln Val Pro 465 470 475 480	2397
cag cct tct gtg agt agc aac ggt atg ctc tac cct gca ctg gcc aag Gln Pro Ser Val Ser Ser Asn Gly Met Leu Tyr Pro Ala Leu Ala Lys 485 490 495	2445
gag agt gga tac ata gcc cct cag gga gca tgc aac aag atg gct acc Glu Ser Gly Tyr Ile Ala Pro Gln Gly Ala Cys Asn Lys Met Ala Thr 500 505 510	2493
att gat gag aat ggg aac cag aat gga tct ggc agg cct ggg ttt gcc Ile Asp Glu Asn Gly Asn Gln Asn Gly Ser Gly Arg Pro Gly Phe Ala 515 520 525	2541
ttc tgc cag ccc tta gaa cat gac ttg ctg tcc cca gtg gag aag aaa Phe Cys Gln Pro Leu Glu His Asp Leu Leu Ser Pro Val Glu Lys Lys 530 535 540	2589
cca gaa gct aca gcc aag tat gtc ccc tcc aaa gtc cat ttc tgt tca Pro Glu Ala Thr Ala Lys Tyr Val Pro Ser Lys Val His Phe Cys Ser 545 550 555 560	2637

122257 sequence listing May 10 2006.ST25.txt

gtg cct gaa aat gag gag gat gcc tcc ctg aag aga cat ctc aca cct Val Pro Glu Asn Glu Glu Asp Ala Ser Leu Lys Arg His Leu Thr Pro 565 570 575	2685
ccc caa ggc aac agc cca cat tcc aat gag aga aag agc acc cac agt Pro Gln Gly Asn Ser Pro His Ser Asn Glu Arg Lys Ser Thr His Ser 580 585 590	2733
aac aaa cca tct tct cat ccc cac agc ctc aaa tgc cct cag gct cag Asn Lys Pro Ser Ser His Pro His Ser Leu Lys Cys Pro Gln Ala Gln 595 600 605	2781
gcc tgg caa gcg ggt gaa gac aag aga tct tcc agg ctc tca gag ccc Ala Trp Gln Ala Gly Glu Asp Lys Arg Ser Ser Arg Leu Ser Glu Pro 610 615 620	2829
tgg gag ggc gat ttc cag gaa gac cac aat gcc aac ctc tgg agg agg Trp Glu Gly Asp Phe Gln Glu Asp His Asn Ala Asn Leu Trp Arg Arg 625 630 635 640	2877
ctg gag aga gaa ggc cta ggc cag agc ctg tca ggc aac ttt ggc aag Leu Glu Arg Glu Gly Leu Gly Gln Ser Leu Ser Gly Asn Phe Gly Lys 645 650 655	2925
acc aag tca gcc ttc tca tct ctc cag aac att cct gag agt ctg aga Thr Lys Ser Ala Phe Ser Ser Leu Gln Asn Ile Pro Glu Ser Leu Arg 660 665 670	2973
aga cac agc agc ctg gag cta ggc cgg gga acc cag gag ggt tac ccc Arg His Ser Ser Leu Glu Leu Gly Arg Gly Thr Gln Glu Gly Tyr Pro 675 680 685	3021
ggg ggc agg ccc acc tgt gca gtc aac acc aag gca gaa gac cct ggg Gly Gly Arg Pro Thr Cys Ala Val Asn Thr Lys Ala Glu Asp Pro Gly 690 695 700	3069
agg aaa gcc gct cct gac ctc ggg agc cat ctg gac cgg cag gtt tcc Arg Lys Ala Ala Pro Asp Leu Gly Ser His Leu Asp Arg Gln Val Ser 705 710 715 720	3117
tac ccg cgg ccc gag ggg agg acc ggt gcc tcg gct tct ttc aac agc Tyr Pro Arg Pro Glu Gly Arg Thr Gly Ala Ser Ala Ser Phe Asn Ser 725 730 735	3165
aca gac cca agt ccc gaa gag ccg cct gcc ccc tcg cac ccg cac aca Thr Asp Pro Ser Pro Glu Glu Pro Pro Ala Pro Ser His Pro His Thr 740 745 750	3213
tcc agt ctg ggc cgg agg ggg ccc ggc cca ggc agc gcc tcg gct ctt Ser Ser Leu Gly Arg Arg Gly Pro Gly Pro Gly Ser Ala Ser Ala Leu 755 760 765	3261
cag ggc ttt cag tac ggg aag ccc cac tgc tcg gtg ctg gag aag gtc Gln Gly Phe Gln Tyr Gly Lys Pro His Cys Ser Val Leu Glu Lys Val 770 775 780	3309
tcc aaa ttc gag cag cga gag caa ggg agc cag aga ccg agt gtg ggc Ser Lys Phe Glu Gln Arg Glu Gln Gly Ser Gln Arg Pro Ser Val Gly 785 790 795 800	3357
ggc tct ggt ttt ggc cat aac tat agg ccc cac agg acc gtc tca act Gly Ser Gly Phe Gly His Asn Tyr Arg Pro His Arg Thr Val Ser Thr 805 810 815	3405
tcc agt act tct ggg aat gac ttc gag gag aca aaa gca cac att cgt Ser Ser Thr Ser Gly Asn Asp Phe Glu Glu Thr Lys Ala His Ile Arg 820 825 830	3453

## 122257 sequence listing May 10 2006.ST25.txt

ttc tct gag tca gct gaa ccc cta ggc aac ggg gag cag cac ttc aaa Phe Ser Glu Ser Ala Glu Pro Leu Gly Asn Gly Glu Gln His Phe Lys 835 840 845	3501
aac ggg gag ctg aag ttg gaa gag gct tcc cgg cag ccc tgc ggt cag Asn Gly Glu Leu Lys Leu Glu Glu Ala Ser Arg Gln Pro Cys Gly Gln 850 855 860	3549
cag ctg agc gga gga gcg tcg gac agc ggc cgt ggc ccc cag agg ccg Gln Leu Ser Gly Gly Ala Ser Asp Ser Gly Arg Gly Pro Gln Arg Pro 865 870 880	3597
gac gct cgg ctc ctc cgt agc cag agc acc ttc cag ctc tcc agc gag Asp Ala Arg Leu Leu Arg Ser Gln Ser Thr Phe Gln Leu Ser Ser Glu 885 890 895	3645
cca gag agg gag ccc gag tgg cgg gac agg ccc ggc tcg ccc gaa tcg Pro Glu Arg Glu Pro Glu Trp Arg Asp Arg Pro Gly Ser Pro Glu Ser 900 905 910	3693
ccc ctg ctg gat gcc ccc ttc agc cgc gcc tac cgg aac agc atc aag Pro Leu Leu Asp Ala Pro Phe Ser Arg Ala Tyr Arg Asn Ser Ile Lys 915 920 925	3741
gac gca cag tcc cgt gtc ttg ggg gcc acc tcc ttt cga cgt cga gac Asp Ala Gln Ser Arg Val Leu Gly Ala Thr Ser Phe Arg Arg Arg Asp 930 935 940	3789
ctg gag ctg ggg gcg ccc gtg gcg tcg agg tcc tgg cgg cca cgg cct Leu Glu Leu Gly Ala Pro Val Ala Ser Arg Ser Trp Arg Pro Arg Pro 945 950 955 960	3837
tcc tcg gcc cac gtg ggg ctg cgg agc ccc gag gcg tcg gcc tcc gcc Ser Ser Ala His Val Gly Leu Arg Ser Pro Glu Ala Ser Ala Ser Ala 965 970 975	3885
tcc ccg cac acg ccc cgg gag cgg cac agc gtg acc cct gct gag ggc Ser Pro His Thr Pro Arg Glu Arg His Ser Val Thr Pro Ala Glu Gly 980 985 990	3933
gac ctg gcc agg ccc gtg ccc cct gcc gcc cgg aga ggt gct cgc cgg Asp Leu Ala Arg Pro Val Pro Pro Ala Ala Arg Arg Gly Ala Arg Arg 995 1000 1005	3981
cgc ctg act ccc gag cag aag aag cgc tcc tac tcg gag ccc gag Arg Leu Thr Pro Glu Gln Lys Lys Arg Ser Tyr Ser Glu Pro Glu 1010 1015 1020	4026
aag atg aac gag gtg ggg atc gtg gag gag gcc gaa ccg gca ccc Lys Met Asn Glu Val Gly Ile Val Glu Glu Ala Glu Pro Ala Pro 1025 1030 1035	4071
ctg ggc ccg cag aga aat ggg atg cgt ttc ccg gag agc agc gtg Leu Gly Pro Gln Arg Asn Gly Met Arg Phe Pro Glu Ser Ser Val 1040 1045 1050	4116
gcc gac cgg cgc cgt ctc ttc gag cgc gat ggc aag gcc tgc tcc Ala Asp Arg Arg Arg Leu Phe Glu Arg Asp Gly Lys Ala Cys Ser 1055 1060 1065	4161
acg ctc agc ctg tcg ggg ccc gag ctg aag cag ttc cag cag agc Thr Leu Ser Leu Ser Gly Pro Glu Leu Lys Gln Phe Gln Gln Ser 1070 1075 1080	4206
gcc ctg gcg gac tac atc cag cgc aag acc ggc aag cgg cct acc Ala Leu Ala Asp Tyr Ile Gln Arg Lys Thr Gly Lys Arg Pro Thr 1085 1090 1095	4251

122257 sequence listing May 10 2006.ST25.txt															
tcc Ser	gcc Ala 1100	gcc Ala	ggc Gly	tgc Cys	agc Ser	ctc Leu 1105	cag Gln	gag Glu	ccc Pro	ggg Gly	cca Pro 1110	ctg Leu	cgt Arg	gag Glu	4296
cgc Arg	gcc Ala 1115	cag Gln	agt Ser	gcc Ala	tac Tyr	ctc Leu 1120	cag Gln	ccc Pro	ggc Gly	ccc Pro	gcg Ala 1125	gcg Ala	ctc Leu	gaa Glu	4341
ggc Gly	tcc Ser 1130	ggc Gly	ctc Leu	gcc Ala	tgc Ser	gcc Ala 1135	tcc Ser	agc Ser	ttg Leu	agc Ser	tca Ser 1140	ctg Leu	cgg Arg	gag Glu	4386
ccc Pro	agc Ser 1145	ctg Leu	cag Gln	ccc Pro	cgc Arg	agg Arg 1150	gag Glu	gcc Ala	acg Thr	ctc Leu	ctg Leu 1155	ccg Pro	gcc Ala	aca Thr	4431
gtt Val	gca Ala 1160	gaa Glu	acc Thr	cag Gln	cag Gln	gct Ala 1165	ccc Pro	cga Arg	gat Asp	cgc Arg	agc Ser 1170	agc Ser	tcc Ser	ttc Phe	4476
gcc Ala	ggt Gly 1175	ggc Gly	cgc Arg	cgc Arg	ctc Leu	ggg Gly 1180	gaa Glu	cgg Arg	cga Arg	cgc Arg	ggg Gly 1185	gac Asp	ctg Leu	ctt Leu	4521
agc Ser	gga Gly 1190	gca Ala	aac Asn	ggt Gly	gga Gly	aca Thr 1195	agg Arg	ggc Gly	acc Thr	cag Gln	aga Arg 1200	ggg Gly	gat Asp	gag Glu	4566
acc Thr	ccc Pro 1205	agg Arg	gag Glu	cca Pro	tcc Ser	tcc Ser 1210	tgg Trp	ggg Gly	gcc Ala	agg Arg	gcc Ala 1215	ggg Gly	aag Lys	tcc Ser	4611
atg Met	tcg Ser 1220	gcc Ala	gag Glu	gac Asp	ctg Leu	ctg Leu 1225	gaa Glu	cgc Arg	tcg Ser	gac Asp	gtc Val 1230	ctt Leu	gcg Ala	ggc Gly	4656
cct Pro	gtc Val 1235	cat His	gtg Val	agg Arg	tcc Ser	agg Arg 1240	tca Ser	tct Ser	ccc Pro	gcc Ala	acc Thr 1245	gca Ala	gac Asp	aag Lys	4701
cgc Arg	cag Gln 1250	gat Asp	gtg Val	ctt Leu	ttg Leu	ggg Gly 1255	caa Gln	gac Asp	agt Ser	ggc Gly	ttt Phe 1260	ggg Gly	ctt Leu	gtg Val	4746
aag Lys	gat Asp 1265	cca Pro	tgt Cys	tat Tyr	ttg Leu	gct Ala 1270	ggg Gly	cct Pro	gga Gly	tct Ser	agg Arg 1275	tca Ser	ctc Leu	agt Ser	4791
tgt Cys	tca Ser 1280	gaa Glu	aga Arg	ggc Gly	caa Gln	gaa Glu 1285	gag Glu	atg Met	ctg Leu	ctg Leu	ctc Leu 1290	ttc Phe	cac His	cat His	4836
ctc Leu	acc Thr 1295	cct Pro	cgt Arg	tgg Trp	ggt Gly	ggt Gly 1300	tca Ser	ggc Gly	tgc Cys	aaa Lys	gcc Ala 1305	att Ile	ggt Gly	gat Asp	4881
tcc Ser	tcc Ser 1310	gtt Val	cct Pro	agt Ser	gaa Glu	tgt Cys 1315	cct Pro	gga Gly	acc Thr	ctg Leu	gac Asp 1320	cat His	cag Gln	agg Arg	4926
caa Gln	gcc Ala 1325	agt Ser	agg Arg	aca Thr	ccc Pro	tgc Cys 1330	ccc Pro	agg Arg	cca Pro	cca Pro	ctg Leu 1335	gca Ala	gga Gly	acg Thr	4971
caa Gln	ggg Gly 1340	ctg Leu	gtc Val	aca Thr	gac Asp	acc Thr 1345	agg Arg	gct Ala	gca Ala	ccc Pro	ctg Leu 1350	acc Thr	cca Pro	att Ile	5016

122257 sequence listing May 10 2006.ST25.txt															
ggc Gly	acc Thr 1355	cct Pro	ctg Leu	cct Pro	tca Ser	gcc Ala 1360	att Ile	ccc Pro	tct Ser	ggc Gly	tac Tyr 1365	tgc Cys	tca Ser	cag Gln	5061
gac Asp	ggt Gly 1370	cag Gln	aca Thr	ggg Gly	cga Arg	cag Gln 1375	cct Pro	ctc Leu	ccg Pro	ccc Pro	tac Tyr 1380	acc Thr	cct Pro	gcc Ala	5106
atg Met	atg Met 1385	cac His	aga Arg	agc Ser	aat Asn	ggt Gly 1390	cac His	acc Thr	ctg Leu	acc Thr	cag Gln 1395	cct Pro	ccc Pro	ggt Gly	5151
cca Pro	aga Arg 1400	ggc Gly	tgt Cys	gag Glu	ggc Gly	gat Asp 1405	ggc Gly	cca Pro	gag Glu	cat His	ggg Gly 1410	gta Val	gaa Glu	gag Glu	5196
gga Gly	acg Thr 1415	agg Arg	aag Lys	agg Arg	gtc Val	tcg Ser 1420	ctg Leu	cct Pro	cag Gln	tgg Trp	cca Pro 1425	cct Pro	cct Pro	tct Ser	5241
cga Arg	gca Ala 1430	aag Lys	tgg Trp	gcc Ala	cac His	gca Ala 1435	gcc Ala	aga Arg	gag Glu	gac Asp	agc Ser 1440	ctt Leu	cct Pro	gag Glu	5286
gaa Glu	tcc Ser 1445	tca Ser	gcc Ala	cct Pro	gat Asp	ttt Phe 1450	gca Ala	aac Asn	ctg Leu	aag Lys	cac His 1455	tat Tyr	caa Gln	aaa Lys	5331
cag Gln	cag Gln 1460	agt Ser	ctt Leu	cca Pro	agt Ser	tta Leu 1465	tgc Cys	agc Ser	act Thr	tct Ser	gac Asp 1470	cca Pro	gac Asp	aca Thr	5376
cct Pro	ctt Leu 1475	ggg Gly	gcc Ala	ccg Pro	agc Ser	act Thr 1480	cca Pro	ggg Gly	agg Arg	atc Ile	tcc Ser 1485	ctc Leu	cga Arg	ata Ile	5421
tct Ser	gag Glu 1490	tct Ser	gtc Val	ctg Leu	cgg Arg	gac Asp 1495	tcc Ser	ccg Pro	cca Pro	cct Pro	cat His 1500	gag Glu	gat Asp	tat Tyr	5466
gaa Glu	gac Asp 1505	gaa Glu	gtg Val	ttt Phe	gtg Val	agg Arg 1510	gat Asp	ccg Pro	cac His	ccc Pro	aag Lys 1515	gcc Ala	acg Thr	tcc Ser	5511
agc Ser	ccc Pro 1520	aca Thr	ttt Phe	gaa Glu	cct Pro	ctt Leu 1525	ccc Pro	cca Pro	ccc Pro	cca Pro	cct Pro 1530	cct Pro	cca Pro	ccg Pro	5556
agt Ser	cag Gln 1535	gaa Glu	acc Thr	ccg Pro	gtg Val	tat Tyr 1540	agc Ser	atg Met	gat Asp	gac Asp	ttc Phe 1545	cct Pro	cca Pro	cct Pro	5601
cct Pro	ccc Pro 1550	cac His	act Thr	gta Val	tgt Cys	gag Glu 1555	gcg Ala	cag Gln	ctg Leu	gac Asp	agt Ser 1560	gag Glu	gat Asp	ccc Pro	5646
gag Glu	ggg Gly 1565	cca Pro	cgc Arg	ccc Pro	agc Ser	ttc Phe 1570	aac Asn	aaa Lys	ctt Leu	tct Ser	aaa Lys 1575	gtg Val	aca Thr	att Ile	5691
gca Ala	agg Arg 1580	gaa Glu	agg Arg	cac His	atg Met	cct Pro 1585	ggt Gly	gca Ala	gcc Ala	cat His	gtg Val 1590	gta Val	ggt Gly	agt Ser	5736
cag Gln	aca Thr 1595	ctg Leu	gct Ala	tcc Ser	aga Arg	ctc Leu 1600	caa Gln	act Thr	tct Ser	atc Ile	aag Lys 1605	ggt Gly	tca Ser	gag Glu	5781

122257 sequence listing May 10 2006.ST25.txt															
gct Ala	gag Glu 1610	tcc Ser	aca Thr	cca Pro	ccc Pro	tcc Ser 1615	ttc Phe	atg Met	agc Ser	gtt Val	cac His 1620	gcc Ala	caa Gln	ctt Leu	5826
gct Ala	ggg Gly 1625	tct Ser	ctt Leu	ggg Gly	ggg Gly	cag Gln 1630	cca Pro	gca Ala	ccc Pro	atc Ile	cag Gln 1635	act Thr	caa Gln	agc Ser	5871
ctc Leu	agc Ser 1640	cat His	gat Asp	cca Pro	gtc Val	agt Ser 1645	gga Gly	act Thr	cag Gln	ggg Gly	tta Leu 1650	gaa Glu	aag Lys	aaa Lys	5916
gtc Val	agt Ser 1655	cct Pro	gat Asp	cct Pro	cag Gln	aag Lys 1660	agt Ser	tca Ser	gaa Glu	gac Asp	atc Ile 1665	aga Arg	aca Thr	gag Glu	5961
gct Ala	ttg Leu 1670	gcc Ala	aag Lys	gaa Glu	att Ile	gtc Val 1675	cac His	caa Gln	gac Asp	aaa Lys	tct Ser 1680	cta Leu	gca Ala	gac Asp	6006
att Ile	ttg Leu 1685	gat Asp	cca Pro	gac Asp	tcc Ser	agg Arg 1690	ctg Leu	aag Lys	aca Thr	aca Thr	atg Met 1695	gac Asp	ctg Leu	atg Met	6051
gaa Glu	ggg Gly 1700	ttg Leu	ttt Phe	ccc Pro	cga Arg	gat Asp 1705	gtg Val	aac Asn	ttg Leu	ctg Leu	aag Lys 1710	gaa Glu	aac Asn	agt Ser	6096
gta Val	aag Lys 1715	agg Arg	aag Lys	gcc Ala	ata Ile	cag Gln 1720	aga Arg	act Thr	gtc Val	agc Ser	tct Ser 1725	tca Ser	gga Gly	tgt Cys	6141
gaa Glu	ggc Gly 1730	aag Lys	agg Arg	aat Asn	gaa Glu	gac Asp 1735	aag Lys	gaa Glu	gca Ala	gtg Val	agc Ser 1740	atg Met	ttg Leu	gtt Val	6186
aac Asn	tgc Cys 1745	cct Pro	gcc Ala	tac Tyr	tac Tyr	agt Ser 1750	gtg Val	tct Ser	gct Ala	ccc Pro	aag Lys 1755	gct Ala	gag Glu	cta Leu	6231
ctg Leu	aac Asn 1760	aaa Lys	atc Ile	aaa Lys	gag Glu	atg Met 1765	cca Pro	gca Ala	gaa Glu	gtg Val	aat Asn 1770	gag Glu	gaa Glu	gag Glu	6276
gaa Glu	cag Gln 1775	gca Ala	gat Asp	gtc Val	aat Asn	gaa Glu 1780	aag Lys	aag Lys	gct Ala	gag Glu	ctc Leu 1785	att Ile	gga Gly	agt Ser	6321
ctc Leu	acc Thr 1790	cac His	aag Lys	ctg Leu	gag Glu	acc Thr 1795	ctc Leu	cag Gln	gag Glu	gcg Ala	aag Lys 1800	ggg Gly	agc Ser	ctg Leu	6366
ctc Leu	acg Thr 1805	gac Asp	atc Ile	aag Lys	ctc Leu	aac Asn 1810	aac Asn	gcc Ala	ctg Leu	gga Gly	gaa Glu 1815	gag Glu	gtg Val	gag Glu	6411
gct Ala	ctg Leu 1820	atc Ile	agc Ser	gag Glu	ctc Leu	tgc Cys 1825	aag Lys	ccc Pro	aat Asn	gag Glu	ttt Phe 1830	gac Asp	aag Lys	tat Tyr	6456
agg Arg	atg Met 1835	ttc Phe	ata Ile	ggg Gly	gat Asp	ttg Leu 1840	gac Asp	aag Lys	gtg Val	gtc Val	aac Asn 1845	ctg Leu	ctg Leu	ctc Leu	6501
tcc Ser	ctc Leu 1850	tcg Ser	ggg Gly	cgt Arg	cta Leu	gcc Ala 1855	cgt Arg	gtt Val	gag Glu	aat Asn	gtc Val 1860	ctt Leu	agc Ser	ggc Gly	6546

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ctt ggt gaa gat gcc agt aat gaa gaa agg agc tct ctt tac gag Leu Gly Glu Asp Ala Ser Asn Glu Glu Arg Ser Ser Leu Tyr Glu 1865 1870 1875	6591
aaa agg aag atc ctg gct ggt cag cat gag gat gcc cgg gag ctg Lys Arg Lys Ile Leu Ala Gly Gln His Glu Asp Ala Arg Glu Leu 1880 1885 1890	6636
aag gag aac ctg gat cgc agg gag cga gta gtg ctg ggc atc ttg Lys Glu Asn Leu Asp Arg Glu Arg Val Val Leu Gly Ile Leu 1895 1900 1905	6681
gcc aat tac ctt tca gag gag cag ctc cag gac tac cag cac ttc Ala Asn Tyr Leu Ser Glu Glu Gln Leu Gln Asp Tyr Gln His Phe 1910 1915 1920	6726
gtg aaa atg aag tcc acg ctc ctc att gag caa cgg aag ctg gat Val Lys Met Lys Ser Thr Leu Leu Ile Glu Gln Arg Lys Leu Asp 1925 1930 1935	6771
gac aag atc aag ctg ggc cag gag cag gtc aag tgt ctg ctg gag Asp Lys Ile Lys Leu Gly Gln Glu Gln Val Lys Cys Leu Leu Glu 1940 1945 1950	6816
agc ctg ccc tca gat ttc att ccc aag gct ggg gcc ctg gct ctg Ser Leu Pro Ser Asp Phe Ile Pro Lys Ala Gly Ala Leu Ala Leu 1955 1960 1965	6861
ccc cca aac ctc acg agt gag ccc att cct gct ggg ggc tgt act Pro Pro Asn Leu Thr Ser Glu Pro Ile Pro Ala Gly Gly Cys Thr 1970 1975 1980	6906
ttc agt ggt att ttc cca aca tta acc tct cca ctt taacctcttc Phe Ser Gly Ile Phe Pro Thr Leu Thr Ser Pro Leu 1985 1990 1995	6952
taaaataccc aaccaaaga tcaactgtttc tctcaacact atttaactctg aaaaatgttt	7012
cagtacaaac cactgtttga actatctggg ttattggtgt ttgttcctga tgaaaggaaa	7072
aaaattctct ccaggaggaa gcctttttcc ttcttgccct tcctgattga tcttctgaga	7132
gctcgaatgc tgctggacac gtaccccttt ctattattac tttgtagtag aaagaaagtt	7192
aatgaaactg agaactgatt ggaggggtgt tgatcattta gtttttaaca ggctgaggca	7252
acatggatca gtgtgtgtcc ccctcaggaa tgtatccaca gtggccttcc ttgctggtgg	7312
gcagtgtatc ctgatggcag ggtacaagta ccattaatga agggctctgca acataaagcc	7372
ttaaaaagac acacactaag aaaactgtaa aaccttgaac attgttattt atatttttta	7432
aaatggaaaa gatcactatg tttgttgtgc taaccactta tttgattctg ttttgtggtg	7492
gacatagatg attacgtttg agctttgtat tttgtgaaaa ccttaatgaa atgaattcca	7552
aagat	7557

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 <211> 1995  
 <212> PRT  
 <213> homo sapiens  
 <400> 38

Met Arg Thr Thr Glu Asp Phe His Lys Pro Ser Ala Thr Leu Asn Ser  
1 5 10 15



122257 sequence listing May 10 2006.ST25.txt

Asn Thr Ala Thr Lys Gly Arg Tyr Ile Tyr Leu Glu Ala Phe Leu Glu  
20 25 30

Gly Gly Ala Pro Trp Gly Phe Thr Leu Lys Gly Gly Leu Glu His Gly  
35 40 45

Glu Pro Leu Ile Ile Ser Lys Val Glu Glu Gly Gly Lys Ala Asp Thr  
50 55 60

Leu Ser Ser Lys Leu Gln Ala Gly Asp Glu Val Val His Ile Asn Glu  
65 70 75 80

Val Thr Leu Ser Ser Ser Arg Lys Glu Ala Val Ser Leu Val Lys Gly  
85 90 95

Ser Tyr Lys Thr Leu Arg Leu Val Val Arg Arg Asp Val Cys Thr Asp  
100 105 110

Pro Gly His Ala Asp Thr Gly Ala Ser Asn Phe Val Ser Pro Glu His  
115 120 125

Leu Thr Ser Gly Pro Gln His Arg Lys Ala Ala Trp Ser Gly Gly Val  
130 135 140

Lys Leu Arg Leu Lys His Arg Ser Ser Glu Pro Ala Gly Arg Pro His  
145 150 155 160

Ser Trp His Thr Thr Lys Ser Gly Glu Lys Gln Pro Asp Ala Ser Met  
165 170 175

Met Gln Ile Ser Gln Gly Met Ile Gly Pro Pro Trp His Gln Ser Tyr  
180 185 190

His Ser Ser Ser Ser Thr Ser Asp Leu Ser Asn Tyr Asp His Ala Tyr  
195 200 205

Leu Arg Arg Ser Pro Asp Gln Cys Ser Ser Gln Gly Ser Met Glu Ser  
210 215 220

Leu Glu Pro Ser Gly Ala Tyr Pro Pro Cys His Leu Ser Pro Ala Lys  
225 230 235 240

Ser Thr Gly Ser Ile Asp Gln Leu Ser His Phe His Asn Lys Arg Asp  
245 250 255

Ser Ala Tyr Ser Ser Phe Ser Thr Ser Ser Ser Ile Leu Glu Tyr Pro  
260 265 270

His Pro Gly Ile Ser Ala Arg Glu Arg Ser Gly Ser Met Asp Asn Thr  
275 280 285

122257 sequence listing May 10 2006.ST25.txt

Ser Ala Arg Gly Gly Leu Leu Glu Gly Met Arg Gln Ala Asp Ile Arg  
290 295 300

Tyr Val Lys Thr Val Tyr Asp Thr Arg Arg Gly Val Ser Ala Glu Tyr  
305 310 315 320

Glu Val Asn Ser Ser Ala Leu Leu Leu Gln Gly Arg Glu Ala Arg Ala  
325 330 335

Ser Ala Asn Gly Gln Gly Tyr Asp Lys Trp Ser Asn Ile Pro Arg Gly  
340 345 350

Lys Gly Val Pro Pro Pro Ser Trp Ser Gln Gln Cys Pro Ser Ser Leu  
355 360 365

Glu Thr Ala Thr Asp Asn Leu Pro Pro Lys Val Gly Ala Pro Leu Pro  
370 375 380

Pro Ala Arg Ser Asp Ser Tyr Ala Ala Phe Arg His Arg Glu Arg Pro  
385 390 395 400

Ser Ser Trp Ser Ser Leu Asp Gln Lys Arg Leu Cys Arg Pro Gln Ala  
405 410 415

Asn Ser Leu Gly Ser Leu Lys Ser Pro Phe Ile Glu Glu Gln Leu His  
420 425 430

Thr Val Leu Glu Lys Ser Pro Glu Asn Ser Pro Pro Val Lys Pro Lys  
435 440 445

His Asn Tyr Thr Gln Lys Ala Gln Pro Gly Gln Pro Leu Leu Pro Thr  
450 455 460

Ser Ile Tyr Ala Val Pro Ser Leu Glu Pro His Phe Ala Gln Val Pro  
465 470 475 480

Gln Pro Ser Val Ser Ser Asn Gly Met Leu Tyr Pro Ala Leu Ala Lys  
485 490 495

Glu Ser Gly Tyr Ile Ala Pro Gln Gly Ala Cys Asn Lys Met Ala Thr  
500 505 510

Ile Asp Glu Asn Gly Asn Gln Asn Gly Ser Gly Arg Pro Gly Phe Ala  
515 520 525

Phe Cys Gln Pro Leu Glu His Asp Leu Leu Ser Pro Val Glu Lys Lys  
530 535 540

Pro Glu Ala Thr Ala Lys Tyr Val Pro Ser Lys Val His Phe Cys Ser  
545 550 555 560

122257 sequence listing May 10 2006.ST25.txt

Val Pro Glu Asn Glu Glu Asp Ala Ser Leu Lys Arg His Leu Thr Pro  
565 570 575

Pro Gln Gly Asn Ser Pro His Ser Asn Glu Arg Lys Ser Thr His Ser  
580 585 590

Asn Lys Pro Ser Ser His Pro His Ser Leu Lys Cys Pro Gln Ala Gln  
595 600 605

Ala Trp Gln Ala Gly Glu Asp Lys Arg Ser Ser Arg Leu Ser Glu Pro  
610 615 620

Trp Glu Gly Asp Phe Gln Glu Asp His Asn Ala Asn Leu Trp Arg Arg  
625 630 635 640

Leu Glu Arg Glu Gly Leu Gly Gln Ser Leu Ser Gly Asn Phe Gly Lys  
645 650 655

Thr Lys Ser Ala Phe Ser Ser Leu Gln Asn Ile Pro Glu Ser Leu Arg  
660 665 670

Arg His Ser Ser Leu Glu Leu Gly Arg Gly Thr Gln Glu Gly Tyr Pro  
675 680 685

Gly Gly Arg Pro Thr Cys Ala Val Asn Thr Lys Ala Glu Asp Pro Gly  
690 695 700

Arg Lys Ala Ala Pro Asp Leu Gly Ser His Leu Asp Arg Gln Val Ser  
705 710 715 720

Tyr Pro Arg Pro Glu Gly Arg Thr Gly Ala Ser Ala Ser Phe Asn Ser  
725 730 735

Thr Asp Pro Ser Pro Glu Glu Pro Pro Ala Pro Ser His Pro His Thr  
740 745 750

Ser Ser Leu Gly Arg Arg Gly Pro Gly Pro Gly Ser Ala Ser Ala Leu  
755 760 765

Gln Gly Phe Gln Tyr Gly Lys Pro His Cys Ser Val Leu Glu Lys Val  
770 775 780

Ser Lys Phe Glu Gln Arg Glu Gln Gly Ser Gln Arg Pro Ser Val Gly  
785 790 795 800

Gly Ser Gly Phe Gly His Asn Tyr Arg Pro His Arg Thr Val Ser Thr  
805 810 815

Ser Ser Thr Ser Gly Asn Asp Phe Glu Glu Thr Lys Ala His Ile Arg  
820 825 830

122257 sequence listing May 10 2006.ST25.txt

Phe Ser Glu Ser Ala Glu Pro Leu Gly Asn Gly Glu Gln His Phe Lys  
835 840 845

Asn Gly Glu Leu Lys Leu Glu Glu Ala Ser Arg Gln Pro Cys Gly Gln  
850 855 860

Gln Leu Ser Gly Gly Ala Ser Asp Ser Gly Arg Gly Pro Gln Arg Pro  
865 870 875 880

Asp Ala Arg Leu Leu Arg Ser Gln Ser Thr Phe Gln Leu Ser Ser Glu  
885 890 895

Pro Glu Arg Glu Pro Glu Trp Arg Asp Arg Pro Gly Ser Pro Glu Ser  
900 905 910

Pro Leu Leu Asp Ala Pro Phe Ser Arg Ala Tyr Arg Asn Ser Ile Lys  
915 920 925

Asp Ala Gln Ser Arg Val Leu Gly Ala Thr Ser Phe Arg Arg Arg Asp  
930 935 940

Leu Glu Leu Gly Ala Pro Val Ala Ser Arg Ser Trp Arg Pro Arg Pro  
945 950 955 960

Ser Ser Ala His Val Gly Leu Arg Ser Pro Glu Ala Ser Ala Ser Ala  
965 970 975

Ser Pro His Thr Pro Arg Glu Arg His Ser Val Thr Pro Ala Glu Gly  
980 985 990

Asp Leu Ala Arg Pro Val Pro Pro Ala Ala Arg Arg Gly Ala Arg Arg  
995 1000 1005

Arg Leu Thr Pro Glu Gln Lys Lys Arg Ser Tyr Ser Glu Pro Glu  
1010 1015 1020

Lys Met Asn Glu Val Gly Ile Val Glu Glu Ala Glu Pro Ala Pro  
1025 1030 1035

Leu Gly Pro Gln Arg Asn Gly Met Arg Phe Pro Glu Ser Ser Val  
1040 1045 1050

Ala Asp Arg Arg Arg Leu Phe Glu Arg Asp Gly Lys Ala Cys Ser  
1055 1060 1065

Thr Leu Ser Leu Ser Gly Pro Glu Leu Lys Gln Phe Gln Gln Ser  
1070 1075 1080

Ala Leu Ala Asp Tyr Ile Gln Arg Lys Thr Gly Lys Arg Pro Thr  
1085 1090 1095

122257 sequence listing May 10 2006.ST25.txt

Ser	Ala	Ala	Gly	Cys	Ser	Leu	Gln	Glu	Pro	Gly	Pro	Leu	Arg	Glu
	1100					1105					1110			
Arg	Ala	Gln	Ser	Ala	Tyr	Leu	Gln	Pro	Gly	Pro	Ala	Ala	Leu	Glu
	1115					1120					1125			
Gly	Ser	Gly	Leu	Ala	Ser	Ala	Ser	Ser	Leu	Ser	Ser	Leu	Arg	Glu
	1130					1135					1140			
Pro	Ser	Leu	Gln	Pro	Arg	Arg	Glu	Ala	Thr	Leu	Leu	Pro	Ala	Thr
	1145					1150					1155			
Val	Ala	Glu	Thr	Gln	Gln	Ala	Pro	Arg	Asp	Arg	Ser	Ser	Ser	Phe
	1160					1165					1170			
Ala	Gly	Gly	Arg	Arg	Leu	Gly	Glu	Arg	Arg	Arg	Gly	Asp	Leu	Leu
	1175					1180					1185			
Ser	Gly	Ala	Asn	Gly	Gly	Thr	Arg	Gly	Thr	Gln	Arg	Gly	Asp	Glu
	1190					1195					1200			
Thr	Pro	Arg	Glu	Pro	Ser	Ser	Trp	Gly	Ala	Arg	Ala	Gly	Lys	Ser
	1205					1210					1215			
Met	Ser	Ala	Glu	Asp	Leu	Leu	Glu	Arg	Ser	Asp	Val	Leu	Ala	Gly
	1220					1225					1230			
Pro	Val	His	Val	Arg	Ser	Arg	Ser	Ser	Pro	Ala	Thr	Ala	Asp	Lys
	1235					1240					1245			
Arg	Gln	Asp	Val	Leu	Leu	Gly	Gln	Asp	Ser	Gly	Phe	Gly	Leu	Val
	1250					1255					1260			
Lys	Asp	Pro	Cys	Tyr	Leu	Ala	Gly	Pro	Gly	Ser	Arg	Ser	Leu	Ser
	1265					1270					1275			
Cys	Ser	Glu	Arg	Gly	Gln	Glu	Glu	Met	Leu	Leu	Leu	Phe	His	His
	1280					1285					1290			
Leu	Thr	Pro	Arg	Trp	Gly	Gly	Ser	Gly	Cys	Lys	Ala	Ile	Gly	Asp
	1295					1300					1305			
Ser	Ser	Val	Pro	Ser	Glu	Cys	Pro	Gly	Thr	Leu	Asp	His	Gln	Arg
	1310					1315					1320			
Gln	Ala	Ser	Arg	Thr	Pro	Cys	Pro	Arg	Pro	Pro	Leu	Ala	Gly	Thr
	1325					1330					1335			
Gln	Gly	Leu	Val	Thr	Asp	Thr	Arg	Ala	Ala	Pro	Leu	Thr	Pro	Ile
	1340					1345					1350			

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Gly	Thr	Pro	Leu	Pro	Ser	Ala	Ile	Pro	Ser	Gly	Tyr	Cys	Ser	Gln
	1355					1360					1365			
Asp	Gly	Gln	Thr	Gly	Arg	Gln	Pro	Leu	Pro	Pro	Tyr	Thr	Pro	Ala
	1370					1375					1380			
Met	Met	His	Arg	Ser	Asn	Gly	His	Thr	Leu	Thr	Gln	Pro	Pro	Gly
	1385					1390					1395			
Pro	Arg	Gly	Cys	Glu	Gly	Asp	Gly	Pro	Glu	His	Gly	Val	Glu	Glu
	1400					1405					1410			
Gly	Thr	Arg	Lys	Arg	Val	Ser	Leu	Pro	Gln	Trp	Pro	Pro	Pro	Ser
	1415					1420					1425			
Arg	Ala	Lys	Trp	Ala	His	Ala	Ala	Arg	Glu	Asp	Ser	Leu	Pro	Glu
	1430					1435					1440			
Glu	Ser	Ser	Ala	Pro	Asp	Phe	Ala	Asn	Leu	Lys	His	Tyr	Gln	Lys
	1445					1450					1455			
Gln	Gln	Ser	Leu	Pro	Ser	Leu	Cys	Ser	Thr	Ser	Asp	Pro	Asp	Thr
	1460					1465					1470			
Pro	Leu	Gly	Ala	Pro	Ser	Thr	Pro	Gly	Arg	Ile	Ser	Leu	Arg	Ile
	1475					1480					1485			
Ser	Glu	Ser	Val	Leu	Arg	Asp	Ser	Pro	Pro	Pro	His	Glu	Asp	Tyr
	1490					1495					1500			
Glu	Asp	Glu	Val	Phe	Val	Arg	Asp	Pro	His	Pro	Lys	Ala	Thr	Ser
	1505					1510					1515			
Ser	Pro	Thr	Phe	Glu	Pro	Leu	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	1520					1525					1530			
Ser	Gln	Glu	Thr	Pro	Val	Tyr	Ser	Met	Asp	Asp	Phe	Pro	Pro	Pro
	1535					1540					1545			
Pro	Pro	His	Thr	Val	Cys	Glu	Ala	Gln	Leu	Asp	Ser	Glu	Asp	Pro
	1550					1555					1560			
Glu	Gly	Pro	Arg	Pro	Ser	Phe	Asn	Lys	Leu	Ser	Lys	Val	Thr	Ile
	1565					1570					1575			
Ala	Arg	Glu	Arg	His	Met	Pro	Gly	Ala	Ala	His	Val	Val	Gly	Ser
	1580					1585					1590			
Gln	Thr	Leu	Ala	Ser	Arg	Leu	Gln	Thr	Ser	Ile	Lys	Gly	Ser	Glu
	1595					1600					1605			

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Ala	Glu	Ser	Thr	Pro	Pro	Ser	Phe	Met	Ser	Val	His	Ala	Gln	Leu
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Ala	Gly	Ser	Leu	Gly	Gly	Gln	Pro	Ala	Pro	Ile	Gln	Thr	Gln	Ser
	1625					1630					1635			
Leu	Ser	His	Asp	Pro	Val	Ser	Gly	Thr	Gln	Gly	Leu	Glu	Lys	Lys
	1640					1645					1650			
Val	Ser	Pro	Asp	Pro	Gln	Lys	Ser	Ser	Glu	Asp	Ile	Arg	Thr	Glu
	1655					1660					1665			
Ala	Leu	Ala	Lys	Glu	Ile	Val	His	Gln	Asp	Lys	Ser	Leu	Ala	Asp
	1670					1675					1680			
Ile	Leu	Asp	Pro	Asp	Ser	Arg	Leu	Lys	Thr	Thr	Met	Asp	Leu	Met
	1685					1690					1695			
Glu	Gly	Leu	Phe	Pro	Arg	Asp	Val	Asn	Leu	Leu	Lys	Glu	Asn	Ser
	1700					1705					1710			
Val	Lys	Arg	Lys	Ala	Ile	Gln	Arg	Thr	Val	Ser	Ser	Ser	Gly	Cys
	1715					1720					1725			
Glu	Gly	Lys	Arg	Asn	Glu	Asp	Lys	Glu	Ala	Val	Ser	Met	Leu	Val
	1730					1735					1740			
Asn	Cys	Pro	Ala	Tyr	Tyr	Ser	Val	Ser	Ala	Pro	Lys	Ala	Glu	Leu
	1745					1750					1755			
Leu	Asn	Lys	Ile	Lys	Glu	Met	Pro	Ala	Glu	Val	Asn	Glu	Glu	Glu
	1760					1765					1770			
Glu	Gln	Ala	Asp	Val	Asn	Glu	Lys	Lys	Ala	Glu	Leu	Ile	Gly	Ser
	1775					1780					1785			
Leu	Thr	His	Lys	Leu	Glu	Thr	Leu	Gln	Glu	Ala	Lys	Gly	Ser	Leu
	1790					1795					1800			
Leu	Thr	Asp	Ile	Lys	Leu	Asn	Asn	Ala	Leu	Gly	Glu	Glu	Val	Glu
	1805					1810					1815			
Ala	Leu	Ile	Ser	Glu	Leu	Cys	Lys	Pro	Asn	Glu	Phe	Asp	Lys	Tyr
	1820					1825					1830			
Arg	Met	Phe	Ile	Gly	Asp	Leu	Asp	Lys	Val	Val	Asn	Leu	Leu	Leu
	1835					1840					1845			
Ser	Leu	Ser	Gly	Arg	Leu	Ala	Arg	Val	Glu	Asn	Val	Leu	Ser	Gly
	1850					1855					1860			

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Leu Gly Glu Asp Ala Ser Asn Glu Glu Arg Ser Ser Leu Tyr Glu  
1865 1870 1875

Lys Arg Lys Ile Leu Ala Gly Gln His Glu Asp Ala Arg Glu Leu  
1880 1885 1890

Lys Glu Asn Leu Asp Arg Arg Glu Arg Val Val Leu Gly Ile Leu  
1895 1900 1905

Ala Asn Tyr Leu Ser Glu Glu Gln Leu Gln Asp Tyr Gln His Phe  
1910 1915 1920

Val Lys Met Lys Ser Thr Leu Leu Ile Glu Gln Arg Lys Leu Asp  
1925 1930 1935

Asp Lys Ile Lys Leu Gly Gln Glu Gln Val Lys Cys Leu Leu Glu  
1940 1945 1950

Ser Leu Pro Ser Asp Phe Ile Pro Lys Ala Gly Ala Leu Ala Leu  
1955 1960 1965

Pro Pro Asn Leu Thr Ser Glu Pro Ile Pro Ala Gly Gly Cys Thr  
1970 1975 1980

Phe Ser Gly Ile Phe Pro Thr Leu Thr Ser Pro Leu  
1985 1990 1995

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cagcgctacc tggcggaact ggatttctct cccgcctgcc ggcctgcctg ccacagccgg 180  
actccgccac tccggtagcc tc atg gct gca acc tgt gag att agc aac att 232  
Met Ala Ala Thr Cys Glu Ile Ser Asn Ile  
1 5 10  
ttt agc aac tac ttc agt gcg atg tac agc tcg gag gac tcc acc ctg 280  
Phe Ser Asn Tyr Phe Ser Ala Met Tyr Ser Ser Glu Asp Ser Thr Leu  
15 20 25  
gcc tct gtt ccc cct gct gcc acc ttt ggg gcc gat gac ttg gta ctg 328  
Ala Ser Val Pro Pro Ala Ala Thr Phe Gly Ala Asp Asp Leu Val Leu  
30 35 40  
acc ctg agc aac ccc cag atg tca ttg gag ggt aca gag aag gcc agc 376  
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Thr	Leu	Ser 45	Asn	Pro	Gln	Met	Ser 50	Leu	Glu	Gly	Thr	Glu 55	Lys	Ala	Ser	
tgg	ttg	ggg	gaa	cag	ccc	cag	ttc	tgg	tcg	aag	acg	cag	ggt	ctg	gac	424
Trp	Leu	Gly	Glu	Gln	Pro	Gln	Phe	Trp	Ser	Lys	Thr	Gln	Val	Leu	Asp	
60						65					70					
tgg	atc	agc	tac	caa	gtg	gag	aag	aac	aag	tac	gac	gca	agc	gcc	att	472
Trp	Ile	Ser	Tyr	Gln	Val	Glu	Lys	Asn	Lys	Tyr	Asp	Ala	Ser	Ala	Ile	
75					80					85					90	
gac	ttc	tca	cga	tgt	gac	atg	gat	ggc	gcc	acc	ctc	tgc	aat	tgt	gcc	520
Asp	Phe	Ser	Arg	Cys	Asp	Met	Asp	Gly	Ala	Thr	Leu	Cys	Asn	Cys	Ala	
				95					100					105		
ctt	gag	gag	ctg	cgt	ctg	gtc	ttt	ggg	cct	ctg	ggg	gac	caa	ctc	cat	568
Leu	Glu	Glu	Leu	Arg	Leu	Val	Phe	Gly	Pro	Leu	Gly	Asp	Gln	Leu	His	
			110					115					120			
gcc	cag	ctg	cga	gac	ctc	act	tcc	agc	tct	tct	gat	gag	ctc	agt	tgg	616
Ala	Gln	Leu	Arg	Asp	Leu	Thr	Ser	Ser	Ser	Ser	Asp	Glu	Leu	Ser	Trp	
		125					130					135				
atc	att	gag	ctg	ctg	gag	aag	gat	ggc	atg	gcc	ttc	cag	gag	gcc	cta	664
Ile	Ile	Glu	Leu	Leu	Glu	Lys	Asp	Gly	Met	Ala	Phe	Gln	Glu	Ala	Leu	
	140					145					150					
gac	cca	ggg	ccc	ttt	gac	cag	ggc	agc	ccc	ttt	gcc	cag	gag	ctg	ctg	712
Asp	Pro	Gly	Pro	Phe	Asp	Gln	Gly	Ser	Pro	Phe	Ala	Gln	Glu	Leu	Leu	
155					160					165					170	
gac	gac	ggt	cag	caa	gcc	agc	ccc	tac	cac	ccc	ggc	agc	tgt	ggc	gca	760
Asp	Asp	Gly	Gln	Gln	Ala	Ser	Pro	Tyr	His	Pro	Gly	Ser	Cys	Gly	Ala	
				175					180					185		
gga	gcc	ccc	tcc	ccc	ggc	agc	tct	gac	gtc	tcc	acc	gca	ggg	act	ggt	808
Gly	Ala	Pro	Ser	Pro	Gly	Ser	Ser	Asp	Val	Ser	Thr	Ala	Gly	Thr	Gly	
			190					195					200			
gct	tct	cgg	agc	tcc	cac	tcc	tca	gac	tcc	ggt	gga	agt	gac	gtg	gac	856
Ala	Ser	Arg	Ser	Ser	His	Ser	Ser	Asp	Ser	Gly	Gly	Ser	Asp	Val	Asp	
		205					210					215				
ctg	gat	ccc	act	gat	ggc	aag	ctc	ttc	ccc	agc	gat	ggt	ttt	cgt	gac	904
Leu	Asp	Pro	Thr	Asp	Gly	Lys	Leu	Phe	Pro	Ser	Asp	Gly	Phe	Arg	Asp	
	220					225					230					
tgc	aag	aag	ggg	gat	ccc	aag	cac	ggg	aag	cgg	aaa	cga	ggc	cgg	ccc	952
Cys	Lys	Lys	Gly	Asp	Pro	Lys	His	Gly	Lys	Arg	Lys	Arg	Gly	Arg	Pro	
235					240					245					250	
cga	aag	ctg	agc	aaa	gag	tac	tgg	gac	tgt	ctc	gag	ggc	aag	aag	agc	1000
Arg	Lys	Leu	Ser	Lys	Glu	Tyr	Trp	Asp	Cys	Leu	Glu	Gly	Lys	Lys	Ser	
				255					260					265		
aag	cac	gcg	ccc	aga	ggc	acc	cac	ctg	tgg	gag	ttc	atc	cgg	gac	atc	1048
Lys	His	Ala	Pro	Arg	Gly	Thr	His	Leu	Trp	Glu	Phe	Ile	Arg	Asp	Ile	
			270					275					280			
ctc	atc	cac	ccg	gag	ctc	aac	gag	ggc	ctc	atg	aag	tgg	gag	aat	cgg	1096
Leu	Ile	His	Pro	Glu	Leu	Asn	Glu	Gly	Leu	Met	Lys	Trp	Glu	Asn	Arg	
		285					290					295				
cat	gaa	ggc	gtc	ttc	aag	ttc	ctg	cgc	tcc	gag	gct	gtg	gcc	caa	cta	1144
His	Glu	Gly	Val	Phe	Lys	Phe	Leu	Arg	Ser	Glu	Ala	Val	Ala	Gln	Leu	
	300					305					310					
tgg	ggc	caa	aag	aaa	aag	aac	agc	aac	atg	acc	tac	gag	aag	ctg	agc	1192

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Trp Gly Gln Lys Lys Lys Asn Ser Asn Met Thr Tyr Glu Lys Leu Ser	
315 320 325 330	
cgg gcc atg agg tac tac tac aaa cgg gag atc ctg gaa cgg gtg gat	1240
Arg Ala Met Arg Tyr Tyr Tyr Lys Arg Glu Ile Leu Glu Arg Val Asp	
335 340 345	
ggc cgg cga ctc gtc tac aag ttt ggc aaa aac tca agc ggc tgg aag	1288
Gly Arg Arg Leu Val Tyr Lys Phe Gly Lys Asn Ser Ser Gly Trp Lys	
350 355 360	
gag gaa gag gtt ctc cag agt cgg aac tgagggttgg aactataccc	1335
Glu Glu Glu Val Leu Gln Ser Arg Asn	
365 370	
gggaccaaac tcacggacca ctcgaggcct gcaaacccttc ctgggaggac aggcaggcca	1395
gatggccccct ccactgggga atgctcccag ctgtgctgtg gagagaagct gatgttttgg	1455
tgtattgtca gccatcgtcc ttggactcgg agactatggc ctgcctccc caccctcctc	1515
ttggaattac aagccctggg gtttgaagct gacttttatag ctgcaagtgt atctcctttt	1575
atctggtgcc tcctcaaacc cagtctcaga cactaaatgc agacaacacc ttctcctgc	1635
agacacttgg actgagccaa ggaggcttgg gagggcctag ggagcaccgt gatggagagg	1695
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aacctttgtc ttagctacct gtgtactgaa atttgggcct ttggatcgaa tatgggtcaag	2055
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<400> 40

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1 5 10 15

Ala Met Tyr Ser Ser Glu Asp Ser Thr Leu Ala Ser Val Pro Pro Ala

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Ala Thr Phe Gly Ala Asp Asp Leu Val Leu Thr Leu Ser Asn Pro Gln  
35 40 45

Met Ser Leu Glu Gly Thr Glu Lys Ala Ser Trp Leu Gly Glu Gln Pro  
50 55 60

Gln Phe Trp Ser Lys Thr Gln Val Leu Asp Trp Ile Ser Tyr Gln Val  
65 70 75 80

Glu Lys Asn Lys Tyr Asp Ala Ser Ala Ile Asp Phe Ser Arg Cys Asp  
85 90 95

Met Asp Gly Ala Thr Leu Cys Asn Cys Ala Leu Glu Glu Leu Arg Leu  
100 105 110

Val Phe Gly Pro Leu Gly Asp Gln Leu His Ala Gln Leu Arg Asp Leu  
115 120 125

Thr Ser Ser Ser Ser Asp Glu Leu Ser Trp Ile Ile Glu Leu Leu Glu  
130 135 140

Lys Asp Gly Met Ala Phe Gln Glu Ala Leu Asp Pro Gly Pro Phe Asp  
145 150 155 160

Gln Gly Ser Pro Phe Ala Gln Glu Leu Leu Asp Asp Gly Gln Gln Ala  
165 170 175

Ser Pro Tyr His Pro Gly Ser Cys Gly Ala Gly Ala Pro Ser Pro Gly  
180 185 190

Ser Ser Asp Val Ser Thr Ala Gly Thr Gly Ala Ser Arg Ser Ser His  
195 200 205

Ser Ser Asp Ser Gly Gly Ser Asp Val Asp Leu Asp Pro Thr Asp Gly  
210 215 220

Lys Leu Phe Pro Ser Asp Gly Phe Arg Asp Cys Lys Lys Gly Asp Pro  
225 230 235 240

Lys His Gly Lys Arg Lys Arg Gly Arg Pro Arg Lys Leu Ser Lys Glu  
245 250 255

Tyr Trp Asp Cys Leu Glu Gly Lys Lys Ser Lys His Ala Pro Arg Gly  
260 265 270

Thr His Leu Trp Glu Phe Ile Arg Asp Ile Leu Ile His Pro Glu Leu  
275 280 285

Asn Glu Gly Leu Met Lys Trp Glu Asn Arg His Glu Gly Val Phe Lys  
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290

295

300

Phe Leu Arg Ser Glu Ala Val Ala Gln Leu Trp Gly Gln Lys Lys Lys  
 305 310 315 320

Asn Ser Asn Met Thr Tyr Glu Lys Leu Ser Arg Ala Met Arg Tyr Tyr  
 325 330 335

Tyr Lys Arg Glu Ile Leu Glu Arg Val Asp Gly Arg Arg Leu Val Tyr  
 340 345 350

Lys Phe Gly Lys Asn Ser Ser Gly Trp Lys Glu Glu Glu Val Leu Gln  
 355 360 365

Ser Arg Asn  
 370

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 aggaatccca aggaagctgc ctgaatttgc ctgtatactc tcgttctgcg acttataaag 180  
 gaccagacaa atcaaattag tggttttggt ttccgccagc tgtggatgcc tttgacatt 239  
 atg acc gca gag gat tcc acc gca gcc atg agc agt gac tcg gcc gcc 287  
 Met Thr Ala Glu Asp Ser Thr Ala Ala Met Ser Ser Asp Ser Ala Ala  
 1 5 10 15  
 ggg tcc tcg gcc aag gtg ccc gag ggc gtg gcg ggc gcg ccc aac gag 335  
 Gly Ser Ser Ala Lys Val Pro Glu Gly Val Ala Gly Ala Pro Asn Glu  
 20 25 30  
 gca gca ctg ctg gcg ctg atg gag cgc acg ggc tac agc atg gtg caa 383  
 Ala Ala Leu Leu Ala Leu Met Glu Arg Thr Gly Tyr Ser Met Val Gln  
 35 40 45  
 gag aac ggg cag cgc aag tac ggc ggc cca ccg ccc ggc tgg gag ggc 431  
 Glu Asn Gly Gln Arg Lys Tyr Gly Gly Pro Pro Pro Gly Trp Glu Gly  
 50 55 60  
 ccg cac ccg cag cgt ggc tgc gag gtc ttc gtg ggc aag atc ccg cgc 479  
 Pro His Pro Gln Arg Gly Cys Glu Val Phe Val Gly Lys Ile Pro Arg  
 65 70 75 80  
 gac gtg tac gag gac gag ctg gtg ccc gtg ttc gag gcc gtg ggc cgc 527  
 Asp Val Tyr Glu Asp Glu Leu Val Pro Val Phe Glu Ala Val Gly Arg  
 85 90 95  
 acc tac gag ctg cgc ctc atg atg gac ttt gac ggc aag aac cgc ggc 575  
 Thr Tyr Glu Leu Arg Leu Met Met Asp Phe Asp Gly Lys Asn Arg Gly

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100	105	110	
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cgt gag ctc aac aac tac gag atc cgc ccg ggc cgc ctg ctc ggc gtg Arg Glu Leu Asn Asn Tyr Glu Ile Arg Pro Gly Arg Leu Leu Gly Val 130 135 140			671
tgc tgc agc gtg gac aac tgc cgc ctc ttc atc ggc ggg atc ccc aag Cys Cys Ser Val Asp Asn Cys Arg Leu Phe Ile Gly Gly Ile Pro Lys 145 150 155 160			719
atg aag aag cgc gag gaa atc ctg gag gag att gcc aag gtc acc gag Met Lys Lys Arg Glu Glu Ile Leu Glu Glu Ile Ala Lys Val Thr Glu 165 170 175			767
ggc gtg ctg gac gtg atc gtc tac gcc agc gcg gcc gac aag atg aag Gly Val Leu Asp Val Ile Val Tyr Ala Ser Ala Ala Asp Lys Met Lys 180 185 190			815
aac cgc ggc ttc gcc ttc gtg gag tac gag agc cac cgc gcg gct gcc Asn Arg Gly Phe Ala Phe Val Glu Tyr Glu Ser His Arg Ala Ala Ala 195 200 205			863
atg gct cgc cgc aag ctc atg cct ggc cgc atc cag ctg tgg ggc cac Met Ala Arg Arg Lys Leu Met Pro Gly Arg Ile Gln Leu Trp Gly His 210 215 220			911
cag atc gcc gtg gac tgg gcc gag cct gag atc gac gtg gac gag gac Gln Ile Ala Val Asp Trp Ala Glu Pro Glu Ile Asp Val Asp Glu Asp 225 230 235 240			959
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acc acc gag gac acc atc aag aag agc ttc ggc cag ttc aac ccc ggc Thr Thr Glu Asp Thr Ile Lys Lys Ser Phe Gly Gln Phe Asn Pro Gly 260 265 270			1055
tgc gtg gag cgc gtc aag aag atc cgc gac tac gcc ttc gtg cac ttc Cys Val Glu Arg Val Lys Lys Ile Arg Asp Tyr Ala Phe Val His Phe 275 280 285			1103
acc agc cgc gag gat gcc gtg cat gcc atg aac aac ctc aac ggc act Thr Ser Arg Glu Asp Ala Val His Ala Met Asn Asn Leu Asn Gly Thr 290 295 300			1151
gag ctg gag ggc tcg tgc ctg gag gtc acg ctg gcc aag ccc gtg gac Glu Leu Glu Gly Ser Cys Leu Glu Val Thr Leu Ala Lys Pro Val Asp 305 310 315 320			1199
aag gag cag tac tcg cgc tac cag aag gca gcc agg ggc ggc ggc gcg Lys Glu Gln Tyr Ser Arg Tyr Gln Lys Ala Ala Arg Gly Gly Gly Ala 325 330 335			1247
gct gag gca gcg cag cag ccc agc tac gtg tac tcc tgc gac ccc tac Ala Glu Ala Ala Gln Gln Pro Ser Tyr Val Tyr Ser Cys Asp Pro Tyr 340 345 350			1295
aca ctg gcc tac tac ggc tac ccc tac aac gcg ctc att ggg ccc aac Thr Leu Ala Tyr Tyr Gly Tyr Pro Tyr Asn Ala Leu Ile Gly Pro Asn 355 360 365			1343
agg gac tac ttt gtg aaa gta gcc atc cct gcc att ggg gct cag tat Arg Asp Tyr Phe Val Lys Val Ala Ile Pro Ala Ile Gly Ala Gln Tyr 370 375 380 385 390			1391

## 122257 sequence listing May 10 2006.ST25.txt

370		375		380	
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Ser Met Phe Pro Ala Ala Pro Ala Pro Lys Met Ile Glu Asp Gly Lys					
385 390 395 400					
atc cac aca gtg gag cac atg atc agc ccc att gct gtg cag cca gac	1487				
Ile His Thr Val Glu His Met Ile Ser Pro Ile Ala Val Gln Pro Asp					
405 410 415					
cca gcc agt gct gct gcc gcc gca gcc gcg gcc gca gcc gcc gca gcc	1535				
Pro Ala Ser Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala					
420 425 430					
gct gtc att ccc act gtg tcg acg cca cca cct ttc cag ggc cgc cca	1583				
Ala Val Ile Pro Thr Val Ser Thr Pro Pro Pro Phe Gln Gly Arg Pro					
435 440 445					
ata act cca gta tac acg gtg gct cca aac gtt cag aga att cct act	1631				
Ile Thr Pro Val Tyr Thr Val Ala Pro Asn Val Gln Arg Ile Pro Thr					
450 455 460					
gcc ggg atc tac ggg gcc agt tac gtg cca ttt gct gct cca gct aca	1679				
Ala Gly Ile Tyr Gly Ala Ser Tyr Val Pro Phe Ala Ala Pro Ala Thr					
465 470 475 480					
gcc acg atc gcc aca cta cag aag aac gcg gca gcc gcg gcc gcc gtg	1727				
Ala Thr Ile Ala Thr Leu Gln Lys Asn Ala Ala Ala Ala Ala Val					
485 490 495					
tat gga gga tac gca ggc tac ata cct cag gcc ttc cct gct gct gcc	1775				
Tyr Gly Gly Tyr Ala Gly Tyr Ile Pro Gln Ala Phe Pro Ala Ala Ala					
500 505 510					
att cag gtc ccc atc ccc gac gtc tac cag aca tac tgaggctggt	1821				
Ile Gln Val Pro Ile Pro Asp Val Tyr Gln Thr Tyr					
515 520					
gaccagcacg aagacagacc acacaaacac cactgaagga acgcttgact atttatgaag	1881				
aaggaacatg ttggattcac acatgcaacc tgaaagtga gaatgtagc agatttat	1941				
ctgaattatt ttatatacat gaagttttca ctagtttttt aagactat	2001				
atgcctacgt tcatacat tccaaaagact tgcaatgggt cgtgccttca ttccatct	2061				
taaaaatttg tatgctgtac tacatttgta tagagggttt tgttgttggt ttttaagga	2121				
tatatatttca gtatgaagggt tattttctta acttctgcac tccagagatt tctattt	2181				
agtaccttca ataatatatc aactatatat taaaaaagca cacttgagga gctaggga	2241				
tattttgaaa aatatataca atattttaaag atacaaacag tagtgcttaa aaatact	2301				
taaagcatta ttttaaagggt tatactggaa agtgcaattt taaaatgagt aaaac	2361				
tatttctgct ggcattaagg gttgatgggt ttaccatgta tcatcatggc ggtact	2421				
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gtgccttagc cttaaakatg ccccccactcc cacatctctc accctgtccc ctcctccc	2601				
gattcccaat cccaccgcaa tgtttggtgaa gcctaggact gataagtagc tctgatag	2661				
gagctgggtgg cttttatact tcttctctgg tttttgttgg ggtttgttgt ttcgtt	2721				



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Pro His Pro Gln Arg Gly Cys Glu Val Phe Val Gly Lys Ile Pro Arg  
65 70 75 80

Asp Val Tyr Glu Asp Glu Leu Val Pro Val Phe Glu Ala Val Gly Arg  
85 90 95

Thr Tyr Glu Leu Arg Leu Met Met Asp Phe Asp Gly Lys Asn Arg Gly  
100 105 110

Tyr Ala Phe Val Met Tyr Cys His Lys His Glu Ala Lys Arg Ala Val  
115 120 125

Arg Glu Leu Asn Asn Tyr Glu Ile Arg Pro Gly Arg Leu Leu Gly Val  
130 135 140

Cys Cys Ser Val Asp Asn Cys Arg Leu Phe Ile Gly Gly Ile Pro Lys  
145 150 155 160

Met Lys Lys Arg Glu Glu Ile Leu Glu Glu Ile Ala Lys Val Thr Glu  
165 170 175

Gly Val Leu Asp Val Ile Val Tyr Ala Ser Ala Ala Asp Lys Met Lys  
180 185 190

Asn Arg Gly Phe Ala Phe Val Glu Tyr Glu Ser His Arg Ala Ala Ala  
195 200 205

Met Ala Arg Arg Lys Leu Met Pro Gly Arg Ile Gln Leu Trp Gly His  
210 215 220

Gln Ile Ala Val Asp Trp Ala Glu Pro Glu Ile Asp Val Asp Glu Asp  
225 230 235 240

Val Met Glu Thr Val Lys Ile Leu Tyr Val Arg Asn Leu Met Ile Glu  
245 250 255

Thr Thr Glu Asp Thr Ile Lys Lys Ser Phe Gly Gln Phe Asn Pro Gly  
260 265 270

Cys Val Glu Arg Val Lys Lys Ile Arg Asp Tyr Ala Phe Val His Phe  
275 280 285

Thr Ser Arg Glu Asp Ala Val His Ala Met Asn Asn Leu Asn Gly Thr  
290 295 300

Glu Leu Glu Gly Ser Cys Leu Glu Val Thr Leu Ala Lys Pro Val Asp  
305 310 315 320

Lys Glu Gln Tyr Ser Arg Tyr Gln Lys Ala Ala Arg Gly Gly Gly Ala  
325 330 335



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Ala Glu Ala Ala Gln Gln Pro Ser Tyr Val Tyr Ser Cys Asp Pro Tyr  
340 345 350

Thr Leu Ala Tyr Tyr Gly Tyr Pro Tyr Asn Ala Leu Ile Gly Pro Asn  
355 360 365

Arg Asp Tyr Phe Val Lys Val Ala Ile Pro Ala Ile Gly Ala Gln Tyr  
370 375 380

Ser Met Phe Pro Ala Ala Pro Ala Pro Lys Met Ile Glu Asp Gly Lys  
385 390 395 400

Ile His Thr Val Glu His Met Ile Ser Pro Ile Ala Val Gln Pro Asp  
405 410 415

Pro Ala Ser Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala  
420 425 430

Ala Val Ile Pro Thr Val Ser Thr Pro Pro Pro Phe Gln Gly Arg Pro  
435 440 445

Ile Thr Pro Val Tyr Thr Val Ala Pro Asn Val Gln Arg Ile Pro Thr  
450 455 460

Ala Gly Ile Tyr Gly Ala Ser Tyr Val Pro Phe Ala Ala Pro Ala Thr  
465 470 475 480

Ala Thr Ile Ala Thr Leu Gln Lys Asn Ala Ala Ala Ala Ala Ala Val  
485 490 495

Tyr Gly Gly Tyr Ala Gly Tyr Ile Pro Gln Ala Phe Pro Ala Ala Ala  
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Ile Gln Val Pro Ile Pro Asp Val Tyr Gln Thr Tyr  
515 520

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agccccgagc cctcggcggg ctgcgagcga ctccccggcg atg cct cac aac tcc 175  
Met Pro His Asn Ser  
1 5  
atc aga tct ggc cat gga ggg ctg aac cag ctg gga ggg gcc ttt gtg 223

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Ile	Arg	Ser	Gly	His	Gly	Gly	Leu	Asn	Gln	Leu	Gly	Gly	Ala	Phe	Val		
				10					15					20			
aat	ggc	aga	cct	ctg	ccg	gaa	gtg	gtc	cgc	cag	cgc	atc	gta	gac	ctg		271
Asn	Gly	Arg	Pro	Leu	Pro	Glu	Val	Val	Arg	Gln	Arg	Ile	Val	Asp	Leu		
			25					30					35				
gcc	cac	cag	ggt	gta	agg	ccc	tgc	gac	atc	tct	cgc	cag	ctc	cgc	gtc		319
Ala	His	Gln	Gly	Val	Arg	Pro	Cys	Asp	Ile	Ser	Arg	Gln	Leu	Arg	Val		
		40					45					50					
agc	cat	ggc	tgc	gtc	agc	aag	atc	ctt	ggc	agg	tac	tac	gag	act	ggc		367
Ser	His	Gly	Cys	Val	Ser	Lys	Ile	Leu	Gly	Arg	Tyr	Tyr	Glu	Thr	Gly		
	55					60					65						
agc	atc	cgg	cct	gga	gtg	ata	ggg	ggc	tcc	aag	ccc	aag	gtg	gcc	acc		415
Ser	Ile	Arg	Pro	Gly	Val	Ile	Gly	Gly	Ser	Lys	Pro	Lys	Val	Ala	Thr		
				75						80					85		
ccc	aag	gtg	gtg	gag	aag	att	ggg	gac	tac	aaa	cgc	cag	aac	cct	acc		463
Pro	Lys	Val	Val	Glu	Lys	Ile	Gly	Asp	Tyr	Lys	Arg	Gln	Asn	Pro	Thr		
				90					95					100			
atg	ttt	gcc	tgg	gag	atc	cga	gac	cgg	ctc	ctg	gct	gag	ggc	gtc	tgt		511
Met	Phe	Ala	Trp	Glu	Ile	Arg	Asp	Arg	Leu	Leu	Ala	Glu	Gly	Val	Cys		
			105					110					115				
gac	aat	gac	act	gtg	ccc	agt	gtc	agc	tcc	att	aat	aga	atc	atc	cgg		559
Asp	Asn	Asp	Thr	Val	Pro	Ser	Val	Ser	Ser	Ile	Asn	Arg	Ile	Ile	Arg		
		120					125					130					
acc	aaa	gtg	cag	caa	cca	ttc	aac	ctc	cct	atg	gac	agc	tgc	gtg	gcc		607
Thr	Lys	Val	Gln	Gln	Pro	Phe	Asn	Leu	Pro	Met	Asp	Ser	Cys	Val	Ala		
	135					140					145						
acc	aag	tcc	ctg	agt	ccc	gga	cac	acg	ctg	atc	ccc	agc	tca	gct	gta		655
Thr	Lys	Ser	Leu	Ser	Pro	Gly	His	Thr	Leu	Ile	Pro	Ser	Ser	Ala	Val		
					155				160						165		
act	ccc	ccg	gag	tca	ccc	cag	tcg	gat	tcc	ctg	ggc	tcc	acc	tac	tcc		703
Thr	Pro	Pro	Glu	Ser	Pro	Gln	Ser	Asp	Ser	Leu	Gly	Ser	Thr	Tyr	Ser		
				170					175					180			
atc	aat	ggg	ctc	ctg	ggc	atc	gct	cag	cct	ggc	agc	gac	aag	agg	aaa		751
Ile	Asn	Gly	Leu	Leu	Gly	Ile	Ala	Gln	Pro	Gly	Ser	Asp	Lys	Arg	Lys		
			185					190					195				
atg	gat	gac	agt	gat	cag	gat	agc	tgc	cga	cta	agc	att	gac	tca	cag		799
Met	Asp	Asp	Ser	Asp	Gln	Asp	Ser	Cys	Arg	Leu	Ser	Ile	Asp	Ser	Gln		
		200				205						210					
agc	agc	agc	agc	gga	ccc	cga	aag	cac	ctt	cgc	acg	gat	gcc	ttc	agc		847
Ser	Ser	Ser	Ser	Gly	Pro	Arg	Lys	His	Leu	Arg	Thr	Asp	Ala	Phe	Ser		
					220						225						
cag	cac	cac	ctc	gag	ccg	ctc	gag	tgc	cca	ttt	gag	cgg	cag	cac	tac		895
Gln	His	His	Leu	Glu	Pro	Leu	Glu	Cys	Pro	Phe	Glu	Arg	Gln	His	Tyr		
					235					240					245		
cca	gag	gcc	tat	gcc	tcc	ccc	agc	cac	acc	aaa	ggc	gag	cag	ggc	ctc		943
Pro	Glu	Ala	Tyr	Ala	Ser	Pro	Ser	His	Thr	Lys	Gly	Glu	Gln	Gly	Leu		
				250					255					260			
tac	ccg	ctg	ccc	ttg	ctc	aac	agc	acc	ctg	gac	gac	ggg	aag	gcc	acc		991
Tyr	Pro	Leu	Pro	Leu	Leu	Asn	Ser	Thr	Leu	Asp	Asp	Gly	Lys	Ala	Thr		
			265					270					275				
ctg	acc	cct	tcc	aac	acg	cca	ctg	ggg	cgc	aac	ctc	tcg	act	cac	cag		1039

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Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn Leu Ser Thr His Gln	
280 285 290	
acc tac ccc gtg gtg gca gct ccg ccc ttt tgg atc tgc agc aag tcg	1087
Thr Tyr Pro Val Val Ala Ala Pro Pro Phe Trp Ile Cys Ser Lys Ser	
295 300 305	
gct ccg ggg tcc cgc cct tca atg cct ttc ccc atg ctg cct ccg tgt	1135
Ala Pro Gly Ser Arg Pro Ser Met Pro Phe Pro Met Leu Pro Pro Cys	
310 315 320 325	
acg ggc agt tca cgg gcc agg ccc tcc tct cag ggc gag aga tgg tgg	1183
Thr Gly Ser Ser Arg Ala Arg Pro Ser Ser Gln Gly Glu Arg Trp Trp	
330 335 340	
ggc cca cgc tgc ccg gat acc cac ccc aca tcc cca cca gcg gac agg	1231
Gly Pro Arg Cys Pro Asp Thr His Pro Thr Ser Pro Pro Ala Asp Arg	
345 350 355	
gca gct atg cct cct ctg cca tcg cag gca tgg tgg cag gaa gtg aat	1279
Ala Ala Met Pro Pro Leu Pro Ser Gln Ala Trp Trp Gln Glu Val Asn	
360 365 370	
act ctg gca atg cct atg gcc aca ccc cct act cct cct aca gcg agg	1327
Thr Leu Ala Met Pro Met Ala Thr Pro Pro Thr Pro Pro Thr Ala Arg	
375 380 385	
cct ggg gct tcc cca act cca gct tgc tgagttcccc atattattac	1374
Pro Gly Ala Ser Pro Thr Pro Ala Cys	
390 395	
agttccacat caaggccgag tgcaccgccc accactgccca cggcctttga ccattctgtag	1434
ttgccatggg gacagtg	1451

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 <212> PRT  
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<400> 44

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Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser	
35 40 45	
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg	
50 55 60	
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys	
65 70 75 80	
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys	
85 90 95	
Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu	

Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile  
115 120 125

Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met  
130 135 140

Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile  
145 150 155 160

Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu  
165 170 175

Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly  
180 185 190

Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu  
195 200 205

Ser Ile Asp Ser Gln Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg  
210 215 220

Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe  
225 230 235 240

Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys  
245 250 255

Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp  
260 265 270

Asp Gly Lys Ala Thr Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn  
275 280 285

Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Ala Pro Pro Phe Trp  
290 295 300

Ile Cys Ser Lys Ser Ala Pro Gly Ser Arg Pro Ser Met Pro Phe Pro  
305 310 315 320

Met Leu Pro Pro Cys Thr Gly Ser Ser Arg Ala Arg Pro Ser Ser Gln  
325 330 335

Gly Glu Arg Trp Trp Gly Pro Arg Cys Pro Asp Thr His Pro Thr Ser  
340 345 350

Pro Pro Ala Asp Arg Ala Ala Met Pro Pro Leu Pro Ser Gln Ala Trp  
355 360 365

Trp Gln Glu Val Asn Thr Leu Ala Met Pro Met Ala Thr Pro Pro Thr  
Page 116

370

375

380

Pro Pro Thr Ala Arg Pro Gly Ala Ser Pro Thr Pro Ala Cys  
 385 390 395

<210> 45  
 <211> 326  
 <212> DNA  
 <213> homo sapiens

<400> 45  
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 gcaggtggtt gcggtcacia agagaaatca tcaagaatgt tcaacttgga tgtgtgaaag 180  
 attcagggggg tctgcagctg tttagtgttg atgcagttgg gtcaaaagag tatcatgtta 240  
 gtcttctgtg ggttttaggg agggattatg gagcctccct cccacccacac tggctttctt 300  
 gtgtcacagc ctttatttct actccg 326

<210> 46  
 <211> 1534  
 <212> DNA  
 <213> homo sapiens

<220>  
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 <222> (267)..(938)

<400> 46  
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 gtgatgcgcg cggaccagcc cgcgacgccc gggctgccgc tgtccccgca cctggacgct 180  
 ggcgcggttg ccgcgcccc gacctgatcg ctgcgcgcgg cgactcggcc ccaggcttcc 240  
 ggcgcggttg ggggcccctg ctctcc atg ggg ctg agg gac tgg ctg aga acc 293  
 Met Gly Leu Arg Asp Trp Leu Arg Thr  
 1 5  
 gtg tgc tgc tgc tgc cgg tgc gag tgc ttg gag gag cgc gcc ctg cct 341  
 Val Cys Cys Cys Cys Arg Cys Glu Cys Leu Glu Glu Arg Ala Leu Pro 25  
 10 15 20  
 gag aag gag ccc ctc gtc agt gat aac aat cca tat tcc tca ttt gga 389  
 Glu Lys Glu Pro Leu Val Ser Asp Asn Asn Pro Tyr Ser Ser Phe Gly 40  
 30 35 40  
 gca act ctg gtg agg gat gat gag aag aat tta tgg agt atg ccc cat 437  
 Ala Thr Leu Val Arg Asp Asp Glu Lys Asn Leu Trp Ser Met Pro His 55  
 45 50 55  
 gat gtg tcc cac aca gag gca gac gac gac aga acc ctg tac aat ttg 485  
 Asp Val Ser His Thr Glu Ala Asp Asp Asp Arg Thr Leu Tyr Asn Leu 70  
 60 65 70  
 ata gtc att cgt aat cag cag gcc aaa gac tca gag gag tgg cag aag 533  
 Ile Val Ile Arg Asn Gln Gln Ala Lys Asp Ser Glu Glu Trp Gln Lys 85  
 75 80 85

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ctc aac tat gat atc cat acc ctg cgg cag gtt cga agg gaa gta aga Leu Asn Tyr Asp Ile His Thr Leu Arg Gln Val Arg Arg Glu Val Arg 90 95 100 105	581
aac aga tgg aag tgc atc tta gaa gat tta ggt ttt caa aag gaa gct Asn Arg Trp Lys Cys Ile Leu Glu Asp Leu Gly Phe Gln Lys Glu Ala 110 115 120	629
gac tct ttg ttg tca gtg act aaa ctg agc acc atc agt gat tct aaa Asp Ser Leu Leu Ser Val Thr Lys Leu Ser Thr Ile Ser Asp Ser Lys 125 130 135	677
aac aca agg aaa gct cga gag atg ttg tta aaa ctg gct gaa gaa acc Asn Thr Arg Lys Ala Arg Glu Met Leu Leu Lys Leu Ala Glu Glu Thr 140 145 150	725
agt att ttc cca aca agt tgg gag ctg tca gag aga tat ctg ttt gtt Ser Ile Phe Pro Thr Ser Trp Glu Leu Ser Glu Arg Tyr Leu Phe Val 155 160 165	773
gtg gac cgt ctg att gca ctt gat gct gca gaa gag ttc ttt aag ctt Val Asp Arg Leu Ile Ala Leu Asp Ala Ala Glu Glu Phe Phe Lys Leu 170 175 180 185	821
gct cgt cga act tac ccc aag aag cct ggg gtt cca tgc ctg gca gat Ala Arg Arg Thr Tyr Pro Lys Lys Pro Gly Val Pro Cys Leu Ala Asp 190 195 200	869
ggc cag aaa gaa ctg cac ctg tgg ggg gac ctg tca tgc aga ctt gca Gly Gln Lys Glu Leu His Leu Trp Gly Asp Leu Ser Cys Arg Leu Ala 205 210 215	917
cat atg cag gga gta ttg cac tgaagatctt tgctggacct tcttctcttc His Met Gln Gly Val Leu His 220	968
agaagataat tttcaaaagg gagcaatgct gtgaatgcag cttgcttctc tctacagatt	1028
gagaagtcca gcttcaaaag ttacttgcca cttaagcaag gaacttgatca agagatcatg	1088
gttcatgtta ctgaaaagac tttaaggatt tgtaagggtta atccatagat tgctgagaac	1148
aatggaaata tttttatttt tacagatttt gcacttctga attcagggtta aaaactaact	1208
tgtatttagt ctgcttagag gactgtgact tgaaaatttt tatataccaa tgagcttttt	1268
ggtagcgtcc acaatgttta aaatatttca taggcgagat ccgtgttctc catttattaa	1328
tgcatgttag accaatttaa ctgctgtgtt tcaggaaaat tcttcctagt ttaataagca	1388
agctaaaagt tttatttttt atatttagtg cttaatcttt gcctcatgtt atgtaaaatt	1448
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aaacaaacaa taaaataaat aaacct	1534

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<400> 47

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Glu Cys Leu Glu Glu Arg Ala Leu Pro Glu Lys Glu Pro Leu Val Ser  
20 25 30

Asp Asn Asn Pro Tyr Ser Ser Phe Gly Ala Thr Leu Val Arg Asp Asp  
35 40 45

Glu Lys Asn Leu Trp Ser Met Pro His Asp Val Ser His Thr Glu Ala  
50 55 60

Asp Asp Asp Arg Thr Leu Tyr Asn Leu Ile Val Ile Arg Asn Gln Gln  
65 70 75 80

Ala Lys Asp Ser Glu Glu Trp Gln Lys Leu Asn Tyr Asp Ile His Thr  
85 90 95

Leu Arg Gln Val Arg Arg Glu Val Arg Asn Arg Trp Lys Cys Ile Leu  
100 105 110

Glu Asp Leu Gly Phe Gln Lys Glu Ala Asp Ser Leu Leu Ser Val Thr  
115 120 125

Lys Leu Ser Thr Ile Ser Asp Ser Lys Asn Thr Arg Lys Ala Arg Glu  
130 135 140

Met Leu Leu Lys Leu Ala Glu Glu Thr Ser Ile Phe Pro Thr Ser Trp  
145 150 155 160

Glu Leu Ser Glu Arg Tyr Leu Phe Val Val Asp Arg Leu Ile Ala Leu  
165 170 175

Asp Ala Ala Glu Glu Phe Phe Lys Leu Ala Arg Arg Thr Tyr Pro Lys  
180 185 190

Lys Pro Gly Val Pro Cys Leu Ala Asp Gly Gln Lys Glu Leu His Leu  
195 200 205

Trp Gly Asp Leu Ser Cys Arg Leu Ala His Met Gln Gly Val Leu His  
210 215 220

<210> 48  
<211> 2385  
<212> DNA  
<213> homo sapiens

<220>  
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<222> (71)..(1441)

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aaaatcacaa atg tca aat gat gga aga tcc agg aat cgg gac agg cgc 109  
Met Ser Asn Asp Gly Arg Ser Arg Asn Arg Asp Arg Arg

tac	gat	gag	gtc	cca	agc	gac	ctg	ccc	tat	caa	gat	acc	acc	ata	aga	157
Tyr	Asp	Glu	Val	Pro	Ser	Asp	Leu	Pro	Tyr	Gln	Asp	Thr	Thr	Ile	Arg	
	15					20					25					
acc	cac	cca	att	ctt	cat	gac	agt	gag	cgg	gca	gtg	agc	gct	gat	ccc	205
Thr	His	Pro	Ile	Leu	His	Asp	Ser	Glu	Arg	Ala	Val	Ser	Ala	Asp	Pro	
30					35					40					45	
ttg	cca	cca	ccc	cct	ctc	cca	tta	cag	cca	cca	ttc	ggc	cca	gac	ttc	253
Leu	Pro	Pro	Pro	Pro	Leu	Pro	Leu	Gln	Pro	Pro	Phe	Gly	Pro	Asp	Phe	
				50				55						60		
tac	tca	agt	gac	aca	gaa	gaa	cca	gct	ata	gcg	cca	gat	ctc	aaa	cca	301
Tyr	Ser	Ser	Asp	Thr	Glu	Glu	Pro	Ala	Ile	Ala	Pro	Asp	Leu	Lys	Pro	
			65					70					75			
gta	agg	cgc	ttt	gtc	cct	gac	tcc	tgg	aag	aac	ttt	ttc	aga	ggg	aag	349
Val	Arg	Arg	Phe	Val	Pro	Asp	Ser	Trp	Lys	Asn	Phe	Phe	Arg	Gly	Lys	
		80					85					90				
aaa	aag	gac	ccc	gaa	tgg	gat	aag	ccg	gtg	tct	gat	atc	agg	tac	atc	397
Lys	Lys	Asp	Pro	Glu	Trp	Asp	Lys	Pro	Val	Ser	Asp	Ile	Arg	Tyr	Ile	
	95					100					105					
tcc	gat	gga	gtg	gag	tgt	tca	cca	cca	gcc	tct	cca	gca	aga	cca	aac	445
Ser	Asp	Gly	Val	Glu	Cys	Ser	Pro	Pro	Ala	Ser	Pro	Ala	Arg	Pro	Asn	
110					115					120					125	
cac	cgt	tcg	ccc	ctc	aac	tcc	tgc	aaa	gat	ccc	tac	gga	ggg	tca	gaa	493
His	Arg	Ser	Pro	Leu	Asn	Ser	Cys	Lys	Asp	Pro	Tyr	Gly	Gly	Ser	Glu	
				130					135					140		
gga	acc	ttt	agt	tcc	cgg	aaa	gag	gct	gac	gca	gtg	ttt	ccc	cgg	gat	541
Gly	Thr	Phe	Ser	Ser	Arg	Lys	Glu	Ala	Asp	Ala	Val	Phe	Pro	Arg	Asp	
			145				150						155			
ccc	tat	gga	tct	cta	gac	cga	cac	aca	caa	aca	gtt	cga	aca	tac	agt	589
Pro	Tyr	Gly	Ser	Leu	Asp	Arg	His	Thr	Gln	Thr	Val	Arg	Thr	Tyr	Ser	
		160				165						170				
gag	aag	gtg	gag	gag	tat	aac	ctg	aga	tac	tcc	tac	atg	aag	tcg	tgg	637
Glu	Lys	Val	Glu	Glu	Tyr	Asn	Leu	Arg	Tyr	Ser	Tyr	Met	Lys	Ser	Trp	
	175					180					185					
gca	ggc	ctg	ctg	aga	ata	ctg	ggt	gtg	gtg	gag	ctg	ctt	ttg	ggg	gcc	685
Ala	Gly	Leu	Leu	Arg	Ile	Leu	Gly	Val	Val	Glu	Leu	Leu	Leu	Gly	Ala	
190					195					200					205	
ggt	gtc	ttt	gct	tgt	gtc	aca	gct	tac	att	cac	aag	gac	agt	gag	tgg	733
Gly	Val	Phe	Ala	Cys	Val	Thr	Ala	Tyr	Ile	His	Lys	Asp	Ser	Glu	Trp	
				210					215					220		
tac	aac	ttg	ttt	gga	tat	tca	caa	ccg	tat	ggc	atg	gga	ggc	gtt	ggt	781
Tyr	Asn	Leu	Phe	Gly	Tyr	Ser	Gln	Pro	Tyr	Gly	Met	Gly	Gly	Val	Gly	
			225					230					235			
gga	ttg	ggc	agt	atg	tat	ggg	ggc	tat	tac	tac	act	ggc	cct	aag	acc	829
Gly	Leu	Gly	Ser	Met	Tyr	Gly	Gly	Tyr	Tyr	Tyr	Thr	Gly	Pro	Lys	Thr	
		240				245						250				
cct	ttt	gta	ctc	gtg	gtt	gct	gga	tta	gct	tgg	atc	acc	acc	att	att	877
Pro	Phe	Val	Leu	Val	Val	Ala	Gly	Leu	Ala	Trp	Ile	Thr	Thr	Ile	Ile	
	255					260					265					
att	ctg	gtt	ctt	ggc	atg	tcc	atg	tat	tac	cgg	acc	att	ctt	ctg	gac	925
Ile	Leu	Val	Leu	Gly	Met	Ser	Met	Tyr	Tyr	Arg	Thr	Ile	Leu	Leu	Asp	



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270		275		280		285	
tct aat tgg tgg ccc cta act gaa ttt gga att aac gtt gcc ttg ttt	973						
Ser Asn Trp Trp Pro Leu Thr Glu Phe Gly Ile Asn Val Ala Leu Phe		290		295		300	
att ttg tat atg gcc gca gcc ata gtc tat gtg aat gat acc aac cga	1021						
Ile Leu Tyr Met Ala Ala Ala Ile Val Tyr Val Asn Asp Thr Asn Arg		305		310		315	
ggt ggc ctc tgc tac tat ccg tta ttt aat aca cca gtg aat gca gtg	1069						
Gly Gly Leu Cys Tyr Tyr Pro Leu Phe Asn Thr Pro Val Asn Ala Val		320		325		330	
ttc tgc cgg gta gaa gga gga cag ata gct gca atg atc ttc ctg ttt	1117						
Phe Cys Arg Val Glu Gly Gly Gln Ile Ala Ala Met Ile Phe Leu Phe		335		340		345	
gtc acc atg ata gtt tat ctc att agt gct ttg gtt tgc cta aag tta	1165						
Val Thr Met Ile Val Tyr Leu Ile Ser Ala Leu Val Cys Leu Lys Leu		350		355		360	365
tgg agg cat gag gca gct cgg aga cat aga gaa tat atg gaa caa cag	1213						
Trp Arg His Glu Ala Ala Arg Arg His Arg Glu Tyr Met Glu Gln Gln		370		375		380	
gag ata aat gag cca tca ttg tca tcg aaa agg aaa atg tgt gaa atg	1261						
Glu Ile Asn Glu Pro Ser Leu Ser Ser Lys Arg Lys Met Cys Glu Met		385		390		395	
gcc acc agt ggt gac aga caa aga gac tca gaa gtt aat ttc aag gaa	1309						
Ala Thr Ser Gly Asp Arg Gln Arg Asp Ser Glu Val Asn Phe Lys Glu		400		405		410	
ctg aga aca gca aaa atg aaa cct gaa cta ctg agt gga cac atc ccc	1357						
Leu Arg Thr Ala Lys Met Lys Pro Glu Leu Leu Ser Gly His Ile Pro		415		420		425	
cca cgc cca gct aat ttt ttt gta ttt tta gta gag atg ggg ttt cac	1405						
Pro Arg Pro Ala Asn Phe Phe Val Phe Leu Val Glu Met Gly Phe His		430		435		440	445
cgt gtt agc cag gat gat ctc gat ctc ctg acc tca tgatccaccc	1451						
Arg Val Ser Gln Asp Asp Leu Asp Leu Leu Thr Ser		450		455			
gcctcagcct cccaaagtgt tgggattaca ggcgtgagtc accgcgcca gctggatttg	1511						
cttttctatt ccctttggac atacatgcta cagtcccaca atgtagcatt tccttggaaa	1571						
ctcccttttt tttttttttt gagatggagt ttcgctcttg ttgcccaggc tggagtacag	1631						
tggatatgatc ttggctcact gcagcctctg cctcctgggt tcaagcgatt ctctgcctc	1691						
tgcctcccaa gtagctggga ttacaggcac ccaccaccat gccagctaa ttttttgtat	1751						
ttttagtaga gacaggattt cactatgttg gccaggttgg tctcaagctc ctgacctcag	1811						
atgatctacc agcctcggcc ttctgaagtg ctgggattca ggtgtgagcc actgtgcca	1871						
gcagggatgc ttcattcttc taagaattat cttggctttg gactttattc ataaatgttt	1931						
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tcttgttgga ttttattcag cagcatctat catgtagata aattcccagg ttagcatta	2051						
cagcttctga ctaatatagc tgccattcag acaattaatg ttcaaagagt tttctaaagt	2111						

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gataaaacca aagaaaagca tgtggaaaag cagaagctta gaaagttgtg gtcactgaat 2171  
gcactccctg gtttttattt gtcagtgaaa tctttatgca ttcattgtta atattttaat 2231  
tccatggctt tgtaggctgt gctgtgtctg aaggggtaac acctagggaa acatgaggcc 2291  
ccttatggga ccccccaaat ggaacaactt cactttctct tttatgtatt gagccctgtg 2351  
ttaacatttc acttaagaag agcaccagtg cttt 2385

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<211> 457  
<212> PRT  
<213> homo sapiens

<400> 49

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1 5 10 15

Val Pro Ser Asp Leu Pro Tyr Gln Asp Thr Thr Ile Arg Thr His Pro  
20 25 30

Ile Leu His Asp Ser Glu Arg Ala Val Ser Ala Asp Pro Leu Pro Pro  
35 40 45

Pro Pro Leu Pro Leu Gln Pro Pro Phe Gly Pro Asp Phe Tyr Ser Ser  
50 55 60

Asp Thr Glu Glu Pro Ala Ile Ala Pro Asp Leu Lys Pro Val Arg Arg  
65 70 75 80

Phe Val Pro Asp Ser Trp Lys Asn Phe Phe Arg Gly Lys Lys Lys Asp  
85 90 95

Pro Glu Trp Asp Lys Pro Val Ser Asp Ile Arg Tyr Ile Ser Asp Gly  
100 105 110

Val Glu Cys Ser Pro Pro Ala Ser Pro Ala Arg Pro Asn His Arg Ser  
115 120 125

Pro Leu Asn Ser Cys Lys Asp Pro Tyr Gly Gly Ser Glu Gly Thr Phe  
130 135 140

Ser Ser Arg Lys Glu Ala Asp Ala Val Phe Pro Arg Asp Pro Tyr Gly  
145 150 155 160

Ser Leu Asp Arg His Thr Gln Thr Val Arg Thr Tyr Ser Glu Lys Val  
165 170 175

Glu Glu Tyr Asn Leu Arg Tyr Ser Tyr Met Lys Ser Trp Ala Gly Leu  
180 185 190

Leu Arg Ile Leu Gly Val Val Glu Leu Leu Leu Gly Ala Gly Val Phe  
195 200 205

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Ala Cys Val Thr Ala Tyr Ile His Lys Asp Ser Glu Trp Tyr Asn Leu  
210 215 220

Phe Gly Tyr Ser Gln Pro Tyr Gly Met Gly Gly Val Gly Gly Leu Gly  
225 230 235 240

Ser Met Tyr Gly Gly Tyr Tyr Tyr Thr Gly Pro Lys Thr Pro Phe Val  
245 250 255

Leu Val Val Ala Gly Leu Ala Trp Ile Thr Thr Ile Ile Ile Leu Val  
260 265 270

Leu Gly Met Ser Met Tyr Tyr Arg Thr Ile Leu Leu Asp Ser Asn Trp  
275 280 285

Trp Pro Leu Thr Glu Phe Gly Ile Asn Val Ala Leu Phe Ile Leu Tyr  
290 295 300

Met Ala Ala Ala Ile Val Tyr Val Asn Asp Thr Asn Arg Gly Gly Leu  
305 310 315 320

Cys Tyr Tyr Pro Leu Phe Asn Thr Pro Val Asn Ala Val Phe Cys Arg  
325 330 335

Val Glu Gly Gly Gln Ile Ala Ala Met Ile Phe Leu Phe Val Thr Met  
340 345 350

Ile Val Tyr Leu Ile Ser Ala Leu Val Cys Leu Lys Leu Trp Arg His  
355 360 365

Glu Ala Ala Arg Arg His Arg Glu Tyr Met Glu Gln Gln Glu Ile Asn  
370 375 380

Glu Pro Ser Leu Ser Ser Lys Arg Lys Met Cys Glu Met Ala Thr Ser  
385 390 395 400

Gly Asp Arg Gln Arg Asp Ser Glu Val Asn Phe Lys Glu Leu Arg Thr  
405 410 415

Ala Lys Met Lys Pro Glu Leu Leu Ser Gly His Ile Pro Pro Arg Pro  
420 425 430

Ala Asn Phe Phe Val Phe Leu Val Glu Met Gly Phe His Arg Val Ser  
435 440 445

Gln Asp Asp Leu Asp Leu Leu Thr Ser  
450 455

<210> 50  
<211> 2280

## 122257 sequence listing May 10 2006.ST25.txt

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (64)..(2133)

&lt;400&gt; 50

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acc atg gct ccc tgg cct gaa ttg gga gat gcc cag ccc aac ccc gat      108
   Met Ala Pro Trp Pro Glu Leu Gly Asp Ala Gln Pro Asn Pro Asp
   1          5          10          15
aag tac ctc gaa ggg gcc gca ggt cag cag ccc act gcc cct gat aaa      156
Lys Tyr Leu Glu Gly Ala Ala Gly Gln Gln Pro Thr Ala Pro Asp Lys
          20          25          30
agc aaa gag acc aac aaa aca gat aac act gag gca cct gta acc aag      204
Ser Lys Glu Thr Asn Lys Thr Asp Asn Thr Glu Ala Pro Val Thr Lys
          35          40          45
att gaa ctt ctg ccg tcc tac tcc acg gct aca ctg ata gat gag ccc      252
Ile Glu Leu Leu Pro Ser Tyr Ser Thr Ala Thr Leu Ile Asp Glu Pro
          50          55          60
act gag gtg gat gac ccc tgg aac cta ccc act ctt cag gac tcg ggg      300
Thr Glu Val Asp Asp Pro Trp Asn Leu Pro Thr Leu Gln Asp Ser Gly
          65          70          75
atc aag tgg tca gag aga gac acc aaa ggg aag att ctc tgt ttc ttc      348
Ile Lys Trp Ser Glu Arg Asp Thr Lys Gly Lys Ile Leu Cys Phe Phe
          80          85          90          95
caa ggg att ggg aga ttg att tta ctt ctc gga ttt ctc tac ttt ttc      396
Gln Gly Ile Gly Arg Leu Ile Leu Leu Leu Gly Phe Leu Tyr Phe Phe
          100          105          110
gtg tgc tcc ctg gat att ctt agt agc gcc ttc cag ctg gtt gga gga      444
Val Cys Ser Leu Asp Ile Leu Ser Ser Ala Phe Gln Leu Val Gly Gly
          115          120          125
aaa atg gca gga cag ttc ttc agc aac agc tct att atg tcc aac cct      492
Lys Met Ala Gly Gln Phe Phe Ser Asn Ser Ser Ile Met Ser Asn Pro
          130          135          140
ttg ttg ggg ctg gtg atc ggg gtg ctg gtg acc gtc ttg gtg cag agc      540
Leu Leu Gly Leu Val Ile Gly Val Leu Val Thr Val Leu Val Gln Ser
          145          150          155
tcc agc acc tca acg tcc atc gtt gtc agc atg gtg tcc tct tca ttg      588
Ser Ser Thr Ser Thr Ser Ile Val Val Ser Met Val Ser Ser Ser Leu
          160          165          170          175
ctc act gtt cgg gct gcc atc ccc att atc atg ggg gcc aac att gga      636
Leu Thr Val Arg Ala Ala Ile Pro Ile Ile Met Gly Ala Asn Ile Gly
          180          185          190
acg tca atc acc aac act att gtt gcg ctc atg cag gtg gga gat cg      684
Thr Ser Ile Thr Asn Thr Ile Val Ala Leu Met Gln Val Gly Asp Arg
          195          200          205
agt gag ttc aga aga gct ttt gca gga gcc act gtc cat gac ttc ttc      732
Ser Glu Phe Arg Arg Ala Phe Ala Gly Ala Thr Val His Asp Phe Phe
          210          215          220
aac tgg ctg tcc gtg ttg gtg ctc ttg ccc gtg gag gtg gcc acc cat      780

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Asn	Trp	Leu	Ser	Val	Leu	Val	Leu	Leu	Pro	Val	Glu	Val	Ala	Thr	His	
225						230					235					
tac	ctc	gag	atc	ata	acc	cag	ctt	ata	gtg	gag	agc	ttc	cac	ttc	aag	828
Tyr	Leu	Glu	Ile	Ile	Thr	Gln	Leu	Ile	Val	Glu	Ser	Phe	His	Phe	Lys	
240					245					250					255	
aat	gga	gaa	gat	gcc	cca	gat	ctt	ctg	aaa	gtc	atc	act	aag	ccc	ttc	876
Asn	Gly	Glu	Asp	Ala	Pro	Asp	Leu	Leu	Lys	Val	Ile	Thr	Lys	Pro	Phe	
				260					265					270		
aca	aag	ctc	att	gtc	cag	ctg	gat	aaa	aaa	gtt	atc	agc	caa	att	gca	924
Thr	Lys	Leu	Ile	Val	Gln	Leu	Asp	Lys	Lys	Val	Ile	Ser	Gln	Ile	Ala	
			275					280					285			
atg	aac	gat	gaa	aaa	gcg	aaa	aac	aag	agt	ctt	gtc	aag	att	tgg	tgc	972
Met	Asn	Asp	Glu	Lys	Ala	Lys	Asn	Lys	Ser	Leu	Val	Lys	Ile	Trp	Cys	
		290					295					300				
aaa	act	ttt	acc	aac	aag	acc	cag	att	aac	gtc	act	gtt	ccc	tcg	act	1020
Lys	Thr	Phe	Thr	Asn	Lys	Thr	Gln	Ile	Asn	Val	Thr	Val	Pro	Ser	Thr	
	305					310					315					
gct	aac	tgc	acc	tcc	cct	tcc	ctc	tgt	tgg	acg	gat	ggc	atc	caa	aac	1068
Ala	Asn	Cys	Thr	Ser	Pro	Ser	Leu	Cys	Trp	Thr	Asp	Gly	Ile	Gln	Asn	
320					325					330					335	
tgg	acc	atg	aag	aat	gtg	acc	tac	aag	gag	aac	atc	gcc	aaa	tgc	cag	1116
Trp	Thr	Met	Lys	Asn	Val	Thr	Tyr	Lys	Glu	Asn	Ile	Ala	Lys	Cys	Gln	
				340					345					350		
cat	atc	ttt	gtg	aat	ttc	cac	ctc	ccg	gat	ctt	gct	gtg	ggc	acc	atc	1164
His	Ile	Phe	Val	Asn	Phe	His	Leu	Pro	Asp	Leu	Ala	Val	Gly	Thr	Ile	
			355					360					365			
ttg	ctc	ata	ctc	tcc	ctg	ctg	gtc	ctc	tgt	ggg	tgc	ctg	atc	atg	att	1212
Leu	Leu	Ile	Leu	Ser	Leu	Leu	Val	Leu	Cys	Gly	Cys	Leu	Ile	Met	Ile	
		370					375					380				
gtc	aag	atc	ctg	ggc	tct	gtg	ctc	aag	ggg	cag	gtc	gcc	act	gtc	atc	1260
Val	Lys	Ile	Leu	Gly	Ser	Val	Leu	Lys	Gly	Gln	Val	Ala	Thr	Val	Ile	
	385					390					395					
aag	aag	acc	atc	aac	act	gat	ttc	ccc	ttt	ccc	ttt	gca	tgg	ttg	act	1308
Lys	Lys	Thr	Ile	Asn	Thr	Asp	Phe	Pro	Phe	Pro	Phe	Ala	Trp	Leu	Thr	
400					405					410					415	
ggc	tac	ctg	gcc	atc	ctc	gtc	ggg	gca	ggc	atg	acc	ttc	atc	gta	cag	1356
Gly	Tyr	Leu	Ala	Ile	Leu	Val	Gly	Ala	Gly	Met	Thr	Phe	Ile	Val	Gln	
			420					425						430		
agc	agc	tct	gtg	ttc	acg	tcg	gcc	ttg	acc	ccc	ctg	att	gga	atc	ggc	1404
Ser	Ser	Ser	Val	Phe	Thr	Ser	Ala	Leu	Thr	Pro	Leu	Ile	Gly	Ile	Gly	
			435					440					445			
gtg	ata	acc	att	gag	agg	gct	tat	cca	ctc	acg	ctg	ggc	tcc	aac	atc	1452
Val	Ile	Thr	Ile	Glu	Arg	Ala	Tyr	Pro	Leu	Thr	Leu	Gly	Ser	Asn	Ile	
		450					455					460				
ggc	acc	acc	acc	acc	gcc	atc	ctg	gcc	gcc	tta	gcc	agc	cct	ggc	aat	1500
Gly	Thr	Thr	Thr	Thr	Ala	Ile	Leu	Ala	Ala	Leu	Ala	Ser	Pro	Gly	Asn	
	465					470					475					
gca	ttg	agg	agt	tca	ctc	cag	atc	gcc	ctg	tgc	cac	ttt	ttc	ttc	aac	1548
Ala	Leu	Arg	Ser	Ser	Leu	Gln	Ile	Ala	Leu	Cys	His	Phe	Phe	Phe	Asn	
480					485					490					495	
atc	tcc	ggc	atc	ttg	ctg	tgg	tac	ccg	atc	ccg	ttc	act	cgc	ctg	ccc	1596

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<210> 51
<211> 690
<212> PRT
<213> homo sapiens
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Met Ala Pro Trp Pro Glu Leu Gly Asp Ala Gln Pro Asn Pro Asp Lys  
1 5 10 15

Tyr Leu Glu Gly Ala Ala Gly Gln Gln Pro Thr Ala Pro Asp Lys Ser  
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Lys Glu Thr Asn Lys Thr Asp Asn Thr Glu Ala Pro Val Thr Lys Ile  
35 40 45

Glu Leu Leu Pro Ser Tyr Ser Thr Ala Thr Leu Ile Asp Glu Pro Thr  
50 55 60

Glu Val Asp Asp Pro Trp Asn Leu Pro Thr Leu Gln Asp Ser Gly Ile  
65 70 75 80

Lys Trp Ser Glu Arg Asp Thr Lys Gly Lys Ile Leu Cys Phe Phe Gln  
85 90 95

Gly Ile Gly Arg Leu Ile Leu Leu Leu Gly Phe Leu Tyr Phe Phe Val  
100 105 110

Cys Ser Leu Asp Ile Leu Ser Ser Ala Phe Gln Leu Val Gly Gly Lys  
115 120 125

Met Ala Gly Gln Phe Phe Ser Asn Ser Ser Ile Met Ser Asn Pro Leu  
130 135 140

Leu Gly Leu Val Ile Gly Val Leu Val Thr Val Leu Val Gln Ser Ser  
145 150 155 160

Ser Thr Ser Thr Ser Ile Val Val Ser Met Val Ser Ser Ser Leu Leu  
165 170 175

Thr Val Arg Ala Ala Ile Pro Ile Ile Met Gly Ala Asn Ile Gly Thr  
180 185 190

Ser Ile Thr Asn Thr Ile Val Ala Leu Met Gln Val Gly Asp Arg Ser  
195 200 205

Glu Phe Arg Arg Ala Phe Ala Gly Ala Thr Val His Asp Phe Phe Asn  
210 215 220

Trp Leu Ser Val Leu Val Leu Leu Pro Val Glu Val Ala Thr His Tyr  
225 230 235 240

Leu Glu Ile Ile Thr Gln Leu Ile Val Glu Ser Phe His Phe Lys Asn  
245 250 255

Gly Glu Asp Ala Pro Asp Leu Leu Lys Val Ile Thr Lys Pro Phe Thr  
260 265 270

Lys Leu Ile Val Gln Leu Asp Lys Lys Val Ile Ser Gln Ile Ala Met  
275 280 285

Asn Asp Glu Lys Ala Lys Asn Lys Ser Leu Val Lys Ile Trp Cys Lys  
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 290 295 300

Thr Phe Thr Asn Lys Thr Gln Ile Asn Val Thr Val Pro Ser Thr Ala  
 305 310 315 320

Asn Cys Thr Ser Pro Ser Leu Cys Trp Thr Asp Gly Ile Gln Asn Trp  
 325 330 335

Thr Met Lys Asn Val Thr Tyr Lys Glu Asn Ile Ala Lys Cys Gln His  
 340 345 350

Ile Phe Val Asn Phe His Leu Pro Asp Leu Ala Val Gly Thr Ile Leu  
 355 360 365

Leu Ile Leu Ser Leu Leu Val Leu Cys Gly Cys Leu Ile Met Ile Val  
 370 375 380

Lys Ile Leu Gly Ser Val Leu Lys Gly Gln Val Ala Thr Val Ile Lys  
 385 390 395 400

Lys Thr Ile Asn Thr Asp Phe Pro Phe Pro Phe Ala Trp Leu Thr Gly  
 405 410 415

Tyr Leu Ala Ile Leu Val Gly Ala Gly Met Thr Phe Ile Val Gln Ser  
 420 425 430

Ser Ser Val Phe Thr Ser Ala Leu Thr Pro Leu Ile Gly Ile Gly Val  
 435 440 445

Ile Thr Ile Glu Arg Ala Tyr Pro Leu Thr Leu Gly Ser Asn Ile Gly  
 450 455 460

Thr Thr Thr Thr Ala Ile Leu Ala Ala Leu Ala Ser Pro Gly Asn Ala  
 465 470 475 480

Leu Arg Ser Ser Leu Gln Ile Ala Leu Cys His Phe Phe Phe Asn Ile  
 485 490 495

Ser Gly Ile Leu Leu Trp Tyr Pro Ile Pro Phe Thr Arg Leu Pro Ile  
 500 505 510

Arg Met Ala Lys Gly Leu Gly Asn Ile Ser Ala Lys Tyr Arg Trp Phe  
 515 520 525

Ala Val Phe Tyr Leu Ile Ile Phe Phe Phe Leu Ile Pro Leu Thr Val  
 530 535 540

Phe Gly Leu Ser Leu Ala Gly Trp Arg Val Leu Val Gly Val Gly Val  
 545 550 555 560

Pro Val Val Phe Ile Ile Ile Leu Val Leu Cys Leu Arg Leu Leu Gln



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565 570 575

Ser Arg Cys Pro Arg Val Leu Pro Lys Lys Leu Gln Asn Trp Asn Phe  
580 585 590

Leu Pro Leu Trp Met Arg Ser Leu Lys Pro Trp Asp Ala Val Val Ser  
595 600 605

Lys Phe Thr Gly Cys Phe Gln Met Arg Cys Cys Tyr Cys Cys Arg Val  
610 615 620

Cys Cys Arg Ala Cys Cys Leu Leu Cys Gly Cys Pro Lys Cys Cys Arg  
625 630 635 640

Cys Ser Lys Cys Cys Glu Asp Leu Glu Glu Ala Gln Glu Gly Gln Asp  
645 650 655

Val Pro Val Lys Ala Pro Glu Thr Phe Asp Asn Ile Thr Ile Ser Arg  
660 665 670

Glu Ala Gln Gly Glu Val Pro Ala Ser Asp Ser Lys Thr Glu Cys Thr  
675 680 685

Ala Leu  
690

<210> 52  
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<212> DNA  
<213> homo sapiens

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<221> MISC  
<222> (393)..(393)  
<223> residue at position 393 is A, T, C or G

<220>  
<221> misc\_feature  
<222> (393)..(393)  
<223> n is a, c, g, or t

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agttgctgct gtgaatctga aagacttgaa aagcctccac ctgctgtgtg gacttcacatc 120  
caaggggccc agcctcctct ggactccacc ttggacctca gtgactcaga acttctgcct 180  
ctaagctgct ctaaagtcca gactatggat gtgtttctcta ggccttcagg actctagaat 240  
gtccatatatt atttttatgt tcttggtctt gtgttttagg aaaagtgaat cttgctgttt 300  
tcaataatgt gaatgctatg ttctgggaaa atccactatg acatctaagt tttgtgtaca 360  
gagagatatt tttgcaacta tttccacctt ctncacaac cccccacact ccactccaca 420  
ctcttgagtc tctttaccta atggtctcta cctaattggac cctcgtggcc aaaaagtcca 480

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 <212> DNA  
 <213> homo sapiens

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 <221> CDS  
 <222> (287)..(1183)

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 cggctcactg caacctcctc ctcccagagg tactttctcag ccctctagct ccaactgaga 180  
 acccagccag tcaggaagtc gctacttcgg gaacaccaac caatcagggg gccgtcacct 240  
 gctgaaggag tccttcggcg gctgttggtg cgaggagcctg atcgcg atg ggg aca 295  
 Met Gly Thr  
 1  
 aag gcg caa gtc gag agg aaa ctg ttg tgc ctc ttc ata ttg gcg atc 343  
 Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile Leu Ala Ile  
 5 10 15  
 ctg ttg tgc tcc ctg gca ttg ggc agt gtt aca gtg cac tct tct gaa 391  
 Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His Ser Ser Glu  
 20 25 30 35  
 cct gaa gtc aga att cct gag aat aat cct gtg aag ttg tcc tgt gcc 439  
 Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu Ser Cys Ala  
 40 45 50  
 tac tcg ggc ttt tct tct ccc cgt gtg gag tgg aag ttt gac caa gga 487  
 Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe Asp Gln Gly  
 55 60 65  
 gac acc acc aga ctc gtt tgc tat aat aac aag atc aca gct tcc tat 535  
 Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr Ala Ser Tyr  
 70 75 80  
 gag gac cgg gtg acc ttc ttg cca act ggt atc acc ttc aag tcc gtg 583  
 Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe Lys Ser Val  
 85 90 95  
 aca cgg gaa gac act ggg aca tac act tgt atg gtc tct gag gaa ggc 631  
 Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser Glu Glu Gly  
 100 105 110 115  
 ggc aac agc tat ggg gag gtc aag gtc aag ctc atc gtg ctt gtg cct 679  
 Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val Leu Val Pro  
 120 125 130  
 cca tcc aag cct aca gtt aac atc ccc tcc tct gcc acc att ggg aac 727  
 Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn  
 135 140 145  
 cgg gca gtg ctg aca tgc tca gaa caa gat ggt tcc cca cct tct gaa 775  
 Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu  
 150 155 160  
 tac acc tgg ttc aaa gat ggg ata gtg atg cct acg aat ccc aaa agc 823  
 Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser

## 175

<210>	54
<211>	299
<212>	PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 54

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile  
 1 5 10 15  
 Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His  
 20 25 30  
 Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu  
 35 40 45  
 Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe  
 50 55 60  
 Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
 65 70 75 80  
 Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe  
 85 90 95  
 Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
 100 105 110  
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
 115 120 125  
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
 130 135 140  
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
 145 150 155 160  
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
 165 170 175  
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
 180 185 190  
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
 195 200 205  
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
 210 215 220  
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
 225 230 235 240  
 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly  
 245 250 255

122257 sequence listing May 10 2006.ST25.txt  
Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
260 265 270

Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
290 295

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<210> 55
<211> 2154
<212> DNA
<213> homo sapiens
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<220>  
<221> CDS  
<222> (77)..(1108)

<400> 55																																
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ggctgcgact		tctcta		atg		tct		gct		ttg		gct		gcc		cgg		ctg		ctg		cag		ccc		gcg		112				
				Met		Ser		Ala		Leu		Ala		Ala		Arg		Leu		Leu		Gln		Pro		Ala						
				1						5												10										
cac		agc		tgc		tcc		ctt		cgc		ctt		cgc		cct		ttc		cac		ctc		gcg		gca		gtt		cga		160
His		Ser		Cys		Ser		Leu		Arg		Leu		Arg		Pro		Phe		His		Leu		Ala		Ala		Val		Arg		
				15								20												25								
aat		gaa		gct		gtt		gtc		att		tct		gga		agg		aaa		ctg		gcc		cag		cag		atc		aag		208
Asn		Glu		Ala		Val		Val		Ile		Ser		Gly		Arg		Lys		Leu		Ala		Gln		Gln		Ile		Lys		
		30								35										40												
cag		gaa		gtg		cgg		cag		gag		gta		gaa		gag		tgg		gtg		gcc		tca		ggc		aac		aaa		256
Gln		Glu		Val		Arg		Gln		Glu		Val		Glu		Glu		Trp		Val		Ala		Ser		Gly		Asn		Lys		
		45						50										55												60		
cgg		cca		cac		ctg		agt		gtg		atc		ctg		gtt		ggc		gag		aat		cct		gca		agt		cac		304
Arg		Pro		His		Leu		Ser		Val		Ile		Leu		Val		Gly		Glu		Asn		Pro		Ala		Ser		His		
								65										70										75				
tcc		tat		gtc		ctc		aac		aaa		acc		agg		gca		gct		gca		gtt		gtg		gga		atc		aac		352
Ser		Tyr		Val		Leu		Asn		Lys		Thr		Arg		Ala		Ala		Ala		Val		Val		Gly		Ile		Asn		
				80										85												90						
agt		gag		aca		att		atg		aaa		cca		gct		tca		att		tca		gag		gaa		gaa		ttg		ttg		400
Ser		Glu		Thr		Ile		Met		Lys		Pro		Ala		Ser		Ile		Ser		Glu		Glu		Glu		Leu		Leu		
				95								100												105								
aat		tta		atc		aat		aaa		ctg		aat		aat		gat		gat		aat		gta		gat		ggc		ctc		ctt		448
Asn		Leu		Ile		Asn		Lys		Leu		Asn		Asn		Asp		Asp		Asn		Val		Asp		Gly		Leu		Leu		
		110										115										120										
gtt		cag		ttg		cct		ctt		cca		gag		cat		att		gat		gag		aga		agg		atc		tgc		aat		496
Val		Gln		Leu		Pro		Leu		Pro		Glu		His		Ile		Asp		Glu		Arg		Arg		Ile		Cys		Asn		
		125																														

## 122257 sequence listing May 10 2006.ST25.txt

ggt gtg tgg gaa ata atc aag cga act ggc att cca acc cta ggg aag Gly Val Trp Glu Ile Ile Lys Arg Thr Gly Ile Pro Thr Leu Gly Lys 175 180 185	640
aat gtg gtt gtg gct gga agg tca aaa aac gtt gga atg ccc att gca Asn Val Val Val Ala Gly Arg Ser Lys Asn Val Gly Met Pro Ile Ala 190 195 200	688
atg tta ctg cac aca gat ggg gcg cat gaa cgt ccc gga ggt gat gcc Met Leu Leu His Thr Asp Gly Ala His Glu Arg Pro Gly Gly Asp Ala 205 210 215 220	736
act gtt aca ata tct cat cga tat act ccc aaa gag cag ttg aag aaa Thr Val Thr Ile Ser His Arg Tyr Thr Pro Lys Glu Gln Leu Lys Lys 225 230 235	784
cat aca att ctt gca gat att gta ata tct gct gca ggt att cca aat His Thr Ile Leu Ala Asp Ile Val Ile Ser Ala Ala Gly Ile Pro Asn 240 245 250	832
ctg atc aca gca gat atg atc aag gaa gga gca gca gtc att gat gtg Leu Ile Thr Ala Asp Met Ile Lys Glu Gly Ala Ala Val Ile Asp Val 255 260 265	880
gga ata aat aga gtt cac gat cct gta act gcc aaa ccc aag ttg gtt Gly Ile Asn Arg Val His Asp Pro Val Thr Ala Lys Pro Lys Leu Val 270 275 280	928
gga gat gtg gat ttt gaa gga gtc aga caa aaa gct ggg tat atc act Gly Asp Val Asp Phe Glu Gly Val Arg Gln Lys Ala Gly Tyr Ile Thr 285 290 295 300	976
cca gtt cct gga ggt gtt ggc ccc atg aca gtg gca atg cta atg aag Pro Val Pro Gly Gly Val Gly Pro Met Thr Val Ala Met Leu Met Lys 305 310 315	1024
aat acc att att gct gca aaa aag gtg ctg agg ctt gaa gag cga gaa Asn Thr Ile Ile Ala Ala Lys Lys Val Leu Arg Leu Glu Glu Arg Glu 320 325 330	1072
gtg ctg aag tct aaa gag ctt ggg gta gcc act aat taactactgt Val Leu Lys Ser Lys Glu Leu Gly Val Ala Thr Asn 335 340	1118
gtcttctgtg tcacaaacag cactccaggc cagctcaaga agcaaagcag gccaatagaa	1178
atgcaatatt tttaatttat tctactgaaa tgggttaaaa tgatgccttg tatttattga	1238
aagcttaaat ggggtgggtgt ttctgcacat acctctgcag tacctcacca gggagcattc	1298
cagtatcatg caggggtcctg tgatctagcc aggagcagcc attaacctag tgattaatat	1358
gggagacatt accatatgga ggatggatgc ttcactttgt caagcacctc agttacacat	1418
tcgccttttc taggattgca tttcccaagt gctattgcaa taacagttga tactcatttt	1478
aggtaccaga ctttttgagt tcaactgatc aaaccaaagg aaaagtgttg ctagagaaaa	1538
ttggggaaaa ggtgaaaaag aaaaaatggt agtaattgag cagaaaaaaa ttaatttata	1598
tatgtattga ttggcaacca gatttatcta agtagaactg aattggctag gaaaaaagaa	1658
aaactgcatg ttaatcattt tcctaagctg tccttttgag gcttagtcag ttatttgga	1718
aaatgttttag gattattcct tgctattagt actcatttta tgtatgttac cttcagtaa	1778
gttctcccca ttttagtttt ctaggactga aaggattcct ttctacatta tacatgtgtg	1838

122257 sequence listing May 10 2006.ST25.txt

```

ttgtcatatt tggcttttgc tatatacttt aacttcattg ttaaattttt gtattgtata 1898
gtttcttttg tgtatcttaa aacctatttt tgaaaaacaa acttggcttg ataatcattt 1958
gggcagcttg ggtaagtacg caacttactt ttccaccaaa gaactgtcag cagctgcctg 2018
cttttctgtg atgtatgtat cctgttgact ttccagaaa tttttaaga gtttgagtta 2078
ctattgaatt taatcagact ttctgattaa agggttttct ttctttttta ataaaacaca 2138
tctgtctggt atggta 2154

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<210> 56
<211> 344
<212> PRT
<213> homo sapiens
<400> 56

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Met Ser Ala Leu Ala Ala Arg Leu Leu Gln Pro Ala His Ser Cys Ser
1      5      10
Leu Arg Leu Arg Pro Phe His Leu Ala Ala Val Arg Asn Glu Ala Val
20     25     30
Val Ile Ser Gly Arg Lys Leu Ala Gln Gln Ile Lys Gln Glu Val Arg
35     40     45
Gln Glu Val Glu Glu Trp Val Ala Ser Gly Asn Lys Arg Pro His Leu
50     55     60
Ser Val Ile Leu Val Gly Glu Asn Pro Ala Ser His Ser Tyr Val Leu
65     70     75     80
Asn Lys Thr Arg Ala Ala Ala Val Val Gly Ile Asn Ser Glu Thr Ile
85     90     95
Met Lys Pro Ala Ser Ile Ser Glu Glu Glu Leu Leu Asn Leu Ile Asn
100    105    110
Lys Leu Asn Asn Asp Asp Asn Val Asp Gly Leu Leu Val Gln Leu Pro
115    120    125
Leu Pro Glu His Ile Asp Glu Arg Arg Ile Cys Asn Ala Val Ser Pro
130    135    140
Asp Lys Asp Val Asp Gly Phe His Val Ile Asn Val Gly Arg Met Cys
145    150    155    160
Leu Asp Gln Tyr Ser Met Leu Pro Ala Thr Pro Trp Gly Val Trp Glu
165    170    175
Ile Ile Lys Arg Thr Gly Ile Pro Thr Leu Gly Lys Asn Val Val Val
180    185    190

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122257 sequence listing May 10 2006.ST25.txt

Ala Gly Arg Ser Lys Asn Val Gly Met Pro Ile Ala Met Leu Leu His  
195 200 205

Thr Asp Gly Ala His Glu Arg Pro Gly Gly Asp Ala Thr Val Thr Ile  
210 215 220

Ser His Arg Tyr Thr Pro Lys Glu Gln Leu Lys Lys His Thr Ile Leu  
225 230 235 240

Ala Asp Ile Val Ile Ser Ala Ala Gly Ile Pro Asn Leu Ile Thr Ala  
245 250 255

Asp Met Ile Lys Glu Gly Ala Ala Val Ile Asp Val Gly Ile Asn Arg  
260 265 270

Val His Asp Pro Val Thr Ala Lys Pro Lys Leu Val Gly Asp Val Asp  
275 280 285

Phe Glu Gly Val Arg Gln Lys Ala Gly Tyr Ile Thr Pro Val Pro Gly  
290 295 300

Gly Val Gly Pro Met Thr Val Ala Met Leu Met Lys Asn Thr Ile Ile  
305 310 315 320

Ala Ala Lys Lys Val Leu Arg Leu Glu Glu Arg Glu Val Leu Lys Ser  
325 330 335

Lys Glu Leu Gly Val Ala Thr Asn  
340

<210> 57  
<211> 1117  
<212> DNA  
<213> homo sapiens

<220>  
<221> CDS  
<222> (57)..(1025)

<400> 57  
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Met  
1

gcc tat gtc ccc gca ccg ggc tac cag ccc acc tac aac ccg acg ctg 107  
Ala Tyr Val Pro Ala Pro Gly Tyr Gln Pro Thr Tyr Asn Pro Thr Leu  
5 10 15

cct tac tac cag ccc atc ccg ggc ggg ctc aac gtg gga atg tct gtt 155  
Pro Tyr Tyr Gln Pro Ile Pro Gly Gly Leu Asn Val Gly Met Ser Val  
20 25 30

tac atc caa gga gtg gcc agc gag cac atg aag cgg ttc ttc gtg aac 203  
Tyr Ile Gln Gly Val Ala Ser Glu His Met Lys Arg Phe Phe Val Asn  
35 40 45



## 122257 sequence listing May 10 2006.ST25.txt

ttt	gtg	gtt	ggg	cag	gat	ccg	ggc	tca	gac	gtc	gcc	ttc	cac	ttc	aat	251
Phe	Val	Val	Gly	Gln	Asp	Pro	Gly	Ser	Asp	Val	Ala	Phe	His	Phe	Asn	
50					55					60					65	
ccg	cgg	ttt	gac	ggc	tgg	gac	aag	gtg	gtc	ttc	aac	acg	ttg	cag	ggc	299
Pro	Arg	Phe	Asp	Gly	Trp	Asp	Lys	Val	Val	Phe	Asn	Thr	Leu	Gln	Gly	
				70					75					80		
ggg	aag	tgg	ggc	agc	gag	gag	agg	aag	agg	agc	atg	ccc	ttc	aaa	aag	347
Gly	Lys	Trp	Gly	Ser	Glu	Glu	Arg	Lys	Arg	Ser	Met	Pro	Phe	Lys	Lys	
			85					90					95			
ggt	gcc	gcc	ttt	gag	ctg	gtc	ttc	ata	gtc	ctg	gct	gag	cac	tac	aag	395
Gly	Ala	Ala	Phe	Glu	Leu	Val	Phe	Ile	Val	Leu	Ala	Glu	His	Tyr	Lys	
		100					105					110				
gtg	gtg	gta	aat	gga	aat	ccc	ttc	tat	gag	tac	ggg	cac	cgg	ctt	ccc	443
Val	Val	Val	Asn	Gly	Asn	Pro	Phe	Tyr	Glu	Tyr	Gly	His	Arg	Leu	Pro	
	115					120					125					
cta	cag	atg	gtc	acc	cac	ctg	caa	gtg	gat	ggg	gat	ctg	caa	ctt	caa	491
Leu	Gln	Met	Val	Thr	His	Leu	Gln	Val	Asp	Gly	Asp	Leu	Gln	Leu	Gln	
130					135					140					145	
tca	atc	aac	ttc	atc	gga	ggc	cag	ccc	ctc	cgg	ccc	cag	gga	ccc	ccg	539
Ser	Ile	Asn	Phe	Ile	Gly	Gly	Gln	Pro	Leu	Arg	Pro	Gln	Gly	Pro	Pro	
				150					155					160		
atg	atg	cca	cct	tac	cct	ggt	ccc	gga	cat	tgc	cat	caa	cag	ctg	aac	587
Met	Met	Pro	Pro	Tyr	Pro	Gly	Pro	Gly	His	Cys	His	Gln	Gln	Leu	Asn	
			165					170					175			
agc	ctg	ccc	acc	atg	gaa	gga	ccc	cca	acc	ttc	aac	ccg	cct	gtg	cca	635
Ser	Leu	Pro	Thr	Met	Glu	Gly	Pro	Pro	Thr	Phe	Asn	Pro	Pro	Val	Pro	
		180					185					190				
tat	ttc	ggg	agg	ctg	caa	gga	ggg	ctc	aca	gct	cga	aga	acc	atc	atc	683
Tyr	Phe	Gly	Arg	Leu	Gln	Gly	Gly	Leu	Thr	Ala	Arg	Arg	Thr	Ile	Ile	
	195					200					205					
atc	aag	ggc	tat	gtg	cct	ccc	aca	ggc	aag	agc	ttt	gct	atc	aac	ttc	731
Ile	Lys	Gly	Tyr	Val	Pro	Pro	Thr	Gly	Lys	Ser	Phe	Ala	Ile	Asn	Phe	
210					215					220					225	
aag	gtg	ggc	tcc	tca	ggg	gac	ata	gct	ctg	cac	att	aat	ccc	cgc	atg	779
Lys	Val	Gly	Ser	Ser	Gly	Asp	Ile	Ala	Leu	His	Ile	Asn	Pro	Arg	Met	
				230				235						240		
ggc	aac	ggt	acc	gtg	gtc	cgg	aac	agc	ctt	ctg	aat	ggc	tcg	tgg	gga	827
Gly	Asn	Gly	Thr	Val	Val	Arg	Asn	Ser	Leu	Leu	Asn	Gly	Ser	Trp	Gly	
			245					250					255			
tcc	gag	gag	aag	aag	atc	acc	cac	aac	cca	ttt	ggt	ccc	gga	cag	ttc	875
Ser	Glu	Glu	Lys	Lys	Ile	Thr	His	Asn	Pro	Phe	Gly	Pro	Gly	Gln	Phe	
		260					265					270				
ttt	gat	ctg	tcc	att	cgc	tgt	ggc	ttg	gat	cgc	ttc	aag	gtt	tac	gcc	923
Phe	Asp	Leu	Ser	Ile	Arg	Cys	Gly	Leu	Asp	Arg	Phe	Lys	Val	Tyr	Ala	
	275					280					285					
aat	ggc	cag	cac	ctc	ttt	gac	ttt	gcc	cat	cgc	ctc	tcg	gcc	ttc	cag	971
Asn	Gly	Gln	His	Leu	Phe	Asp	Phe	Ala	His	Arg	Leu	Ser	Ala	Phe	Gln	
290					295					300					305	
agg	gtg	gac	aca	ttg	gaa	atc	cag	ggt	gat	gtc	acc	ttg	tcc	tat	gtc	1019
Arg	Val	Asp	Thr	Leu	Glu	Ile	Gln	Gly	Asp	Val	Thr	Leu	Ser	Tyr	Val	
				310					315					320		

122257 sequence listing May 10 2006.ST25.txt 1075  
cag atc taatctattc ctggggccat aactcatggg aaaacagaat tatcccctag  
Gln Ile

gactcctttc taagccccta ataaaatgtc tgaggggtgc tc 1117

<210> 58  
<211> 323  
<212> PRT  
<213> homo sapiens

<400> 58

Met Ala Tyr Val Pro Ala Pro Gly Tyr Gln Pro Thr Tyr Asn Pro Thr  
1 5 10 15

Leu Pro Tyr Tyr Gln Pro Ile Pro Gly Gly Leu Asn Val Gly Met Ser  
20 25 30

Val Tyr Ile Gln Gly Val Ala Ser Glu His Met Lys Arg Phe Phe Val  
35 40 45

Asn Phe Val Val Gly Gln Asp Pro Gly Ser Asp Val Ala Phe His Phe  
50 55 60

Asn Pro Arg Phe Asp Gly Trp Asp Lys Val Val Phe Asn Thr Leu Gln  
65 70 75 80

Gly Gly Lys Trp Gly Ser Glu Glu Arg Lys Arg Ser Met Pro Phe Lys  
85 90 95

Lys Gly Ala Ala Phe Glu Leu Val Phe Ile Val Leu Ala Glu His Tyr  
100 105 110

Lys Val Val Val Asn Gly Asn Pro Phe Tyr Glu Tyr Gly His Arg Leu  
115 120 125

Pro Leu Gln Met Val Thr His Leu Gln Val Asp Gly Asp Leu Gln Leu  
130 135 140

Gln Ser Ile Asn Phe Ile Gly Gly Gln Pro Leu Arg Pro Gln Gly Pro  
145 150 155 160

Pro Met Met Pro Pro Tyr Pro Gly Pro Gly His Cys His Gln Gln Leu  
165 170 175

Asn Ser Leu Pro Thr Met Glu Gly Pro Pro Thr Phe Asn Pro Pro Val  
180 185 190

Pro Tyr Phe Gly Arg Leu Gln Gly Gly Leu Thr Ala Arg Arg Thr Ile  
195 200 205

Ile Ile Lys Gly Tyr Val Pro Pro Thr Gly Lys Ser Phe Ala Ile Asn  
210 215 220

122257 sequence listing May 10 2006.ST25.txt

Phe Lys Val Gly Ser Ser Gly Asp Ile Ala Leu His Ile Asn Pro Arg  
225 230 235 240

Met Gly Asn Gly Thr Val Val Arg Asn Ser Leu Leu Asn Gly Ser Trp  
245 250 255

Gly Ser Glu Glu Lys Lys Ile Thr His Asn Pro Phe Gly Pro Gly Gln  
260 265 270

Phe Phe Asp Leu Ser Ile Arg Cys Gly Leu Asp Arg Phe Lys Val Tyr  
275 280 285

Ala Asn Gly Gln His Leu Phe Asp Phe Ala His Arg Leu Ser Ala Phe  
290 295 300

Gln Arg Val Asp Thr Leu Glu Ile Gln Gly Asp Val Thr Leu Ser Tyr  
305 310 315 320

Val Gln Ile

<210> 59  
<211> 3697  
<212> DNA  
<213> homo sapiens

<220>  
<221> CDS  
<222> (121)..(2616)

<400> 59  
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gaaaaggact tttaaccacc attttgtgac ttacagaaag gaatttgaat aaagaaaact 120  
atg ata ctt cag gcc cat ctt cac tcc ctg tgt ctt ctt atg ctt tat 168  
Met Ile Leu Gln Ala His Leu His Ser Leu Cys Leu Leu Met Leu Tyr  
1 5 10 15  
ttg gca act gga tat ggc caa gag ggg aag ttt agt gga ccc ctg aaa 216  
Leu Ala Thr Gly Tyr Gly Gln Glu Gly Lys Phe Ser Gly Pro Leu Lys  
20 25 30  
ccc atg aca ttt tct att tat gaa ggc caa gaa ccg agt caa att ata 264  
Pro Met Thr Phe Ser Ile Tyr Glu Gly Gln Glu Pro Ser Gln Ile Ile  
35 40 45  
ttc cag ttt aag gcc aat cct cct gct gtg act ttt gaa cta act ggg 312  
Phe Gln Phe Lys Ala Asn Pro Pro Ala Val Thr Phe Glu Leu Thr Gly  
50 55 60  
gag aca gac aac ata ttt gtg ata gaa cgg gag gga ctt ctg tat tac 360  
Glu Thr Asp Asn Ile Phe Val Ile Glu Arg Glu Gly Leu Leu Tyr Tyr  
65 70 75 80  
aac aga gcc ttg gac agg gaa aca aga tct act cac aat ctc cag gtt 408  
Asn Arg Ala Leu Asp Arg Glu Thr Arg Ser Thr His Asn Leu Gln Val  
85 90 95

## 122257 sequence listing May 10 2006.ST25.txt

gca gcc ctg gac gct aat gga att ata gtg gag ggt cca gtc cct atc	456
Ala Ala Leu Asp 100 Ala Asn Gly Ile 105 Val Glu Gly Pro Val 110 Pro Ile	
acc ata gaa gtg aag gac atc aac gac aat cga ccc acg ttt ctc cag	504
Thr Ile Glu Val 115 Lys Asp Ile Asn Asp Asn Arg Pro Thr 125 Phe Leu Gln	
tca aag tac gaa ggc tca gta agg cag aac tct cgc cca gga aag ccc	552
Ser Lys 130 Tyr Glu Gly Ser Val 135 Arg Gln Asn Ser Arg 140 Pro Gly Lys Pro	
ttc ttg tat gtc aat gcc aca gac ctg gat gat ccg gcc act ccc aat	600
Phe Leu Tyr Val Asn 150 Ala Thr Asp Leu Asp 155 Pro Ala Thr Pro Asn 160	
ggc cag ctt tat tac cag att gtc atc cag ctt ccc atg atc aac aat	648
Gly Gln Leu Tyr 165 Gln Ile Val Ile 170 Gln Leu Pro Met Ile Asn Asn 175	
gtc atg tac ttt cag atc aac aac aaa acg gga gcc atc tct ctt acc	696
Val Met Tyr Phe 180 Gln Ile Asn Asn Lys 185 Thr Gly Ala Ile Ser 190 Leu Thr	
cga gag gga tct cag gaa ttg aat cct gct aag aat cct tcc tat aat	744
Arg Glu Gly Ser Gln Glu Leu Asn 200 Pro Ala Lys Asn Pro 205 Ser Tyr Asn	
ctg gtg atc tca gtg aag gac atg gga ggc cag agt gag aat tcc ttc	792
Leu Val 210 Ile Ser Val Lys Asp 215 Met Gly Gly Gln Ser 220 Glu Asn Ser Phe	
agt gat acc aca tct gtg gat atc ata gtg aca gag aat att tgg aaa	840
Ser Asp Thr Thr Ser Val 230 Asp Ile Ile Val Thr 235 Glu Asn Ile Trp Lys 240	
gca cca aaa cct gtg gag atg gtg gaa aac tca act gat cct cac ccc	888
Ala Pro Lys Pro Val 245 Glu Met Val Glu Asn Ser Thr Asp Pro His 255 Pro	
atc aaa atc act cag gtg cgg tgg aat gat ccc ggt gca caa tat tcc	936
Ile Lys Ile Thr 260 Gln Val Arg Trp Asn Asp Pro Gly Ala Gln Tyr Ser	
tta gtt gac aaa gag aag ctg cca aga ttc cca ttt tca att gac cag	984
Leu Val 275 Asp Lys Glu Lys Leu Pro 280 Arg Phe Pro Phe Ser 285 Ile Asp Gln	
gaa gga gat att tac gtg act cag ccc ttg gac cga gaa gaa aag gat	1032
Glu Gly 290 Asp Ile Tyr Val Thr 295 Gln Pro Leu Asp Arg 300 Glu Glu Lys Asp	
gca tat gtt ttt tat gca gtt gca aag gat gag tac gga aaa cca ctt	1080
Ala Tyr Val Phe Tyr Ala Val Ala Lys Asp Glu Tyr Gly Lys Pro Leu 320	
tca tat ccg ctg gaa att cat gta aaa gtt aaa gat att aat gat aat	1128
Ser Tyr Pro Leu Glu 325 Ile His Val Lys Val 330 Lys Asp Ile Asn Asp 335 Asn	
cca cct aca tgt ccg tca cca gta acc gta ttt gag gtc cag gag aat	1176
Pro Pro Thr Cys 340 Pro Ser Pro Val Thr 345 Val Phe Glu Val Gln Glu Asn	
gaa cga ctg ggt aac agt atc ggg acc ctt act gca cat gac agg gat	1224
Glu Arg Leu 355 Gly Asn Ser Ile Gly 360 Thr Leu Thr Ala His 365 Asp Arg Asp	

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gaa Glu 370	gaa Glu 370	aat Asn	act Thr	gcc Ala	aac Asn	agt Ser 375	ttt Phe	cta Leu	aac Asn	tac Tyr	agg Arg 380	att Ile	gtg Val	gag Glu	caa Gln	1272
act Thr 385	ccc Pro	aaa Lys	ctt Leu	ccc Pro	atg Met 390	gat Asp	gga Gly	ctc Leu	ttc Phe	cta Leu 395	atc Ile	caa Gln	acc Thr	tat Tyr	gct Ala 400	1320
gga Gly	atg Met	tta Leu	cag Gln 405	tta Leu 405	gct Ala	aaa Lys	cag Gln	tcc Ser	ttg Leu 410	aag Lys	aag Lys	caa Gln	gat Asp	act Thr 415	cct Pro	1368
cag Gln	tac Tyr	aac Asn	tta Leu 420	acg Thr	ata Ile	gag Glu	gtg Val	tct Ser 425	gac Asp	aaa Lys	gat Asp	ttc Phe	aag Lys 430	acc Thr	ctt Leu	1416
tgt Cys	ttt Phe	gtg Val 435	caa Gln	atc Ile	aac Asn	gtt Val	att Ile 440	gat Asp	atc Ile	aat Asn	gat Asp	cag Gln 445	atc Ile	ccc Pro	atc Ile	1464
ttt Phe 450	gaa Glu 450	aaa Lys	tca Ser	gat Asp	tat Tyr	gga Gly 455	aac Asn	ctg Leu	act Thr	ctt Leu	gct Ala 460	gaa Glu	gac Asp	aca Thr	aac Asn	1512
att Ile 465	ggg Gly	tcc Ser	acc Thr	atc Ile	tta Leu 470	acc Thr	atc Ile	cag Gln	gcc Ala	act Thr 475	gat Asp	gct Ala	gat Asp	gag Glu	cca Pro 480	1560
ttt Phe	act Thr	ggg Gly	agt Ser	tct Ser 485	aaa Lys	att Ile	ctg Leu	tat Tyr	cat His 490	atc Ile	ata Ile	aag Lys	gga Gly	gac Asp 495	agt Ser	1608
gag Glu	gga Gly	cgc Arg	ctg Leu 500	ggg Gly	gtt Val	gac Asp	aca Thr	gat Asp 505	ccc Pro	cat His	acc Thr	aac Asn	acc Thr 510	gga Gly	tat Tyr	1656
gtc Val	ata Ile	att Ile 515	aaa Lys	aag Lys	cct Pro	ctt Leu	gat Asp 520	ttt Phe	gaa Glu	aca Thr	gca Ala	gct Ala 525	gtt Val	tcc Ser	aac Asn	1704
att Ile 530	gtg Val	ttc Phe	aaa Lys	gca Ala	gaa Glu	aat Asn 535	cct Pro	gag Glu	cct Pro	cta Leu	gtg Val 540	ttt Phe	ggt Gly	gtg Val	aag Lys	1752
tac Tyr 545	aat Asn	gca Ala	agt Ser	tct Ser	ttt Phe 550	gcc Ala	aag Lys	ttc Phe	acg Thr	ctt Leu 555	att Ile	gtg Val	aca Thr	gat Asp	gtg Val 560	1800
aat Asn	gaa Glu	gca Ala	cct Pro	caa Gln 565	ttt Phe	tcc Ser	caa Gln	cac His	gta Val 570	ttc Phe	caa Gln	gcg Ala	aaa Lys	gtc Val 575	agt Ser	1848
gag Glu	gat Asp	gta Val	gct Ala 580	ata Ile	ggc Gly	act Thr	aaa Lys	gtg Val 585	ggc Gly	aat Asn	gtg Val	act Thr	gcc Ala 590	aag Lys	gat Asp	1896
cca Pro	gaa Glu	ggg Gly 595	ctg Leu	gac Asp	ata Ile	agc Ser	tat Tyr 600	tca Ser	ctg Leu	agg Arg	gga Gly	gac Asp 605	aca Thr	aga Arg	ggg Gly	1944
tgg Trp 610	ctt Leu	aaa Lys	att Ile	gac Asp	cac His	gtg Val 615	act Thr	ggg Gly	gag Glu	atc Ile	ttt Phe 620	agt Ser	gtg Val	gct Ala	cca Pro	1992
ttg Leu 625	gac Asp	aga Arg	gaa Glu	gcc Ala	gga Gly 630	agt Ser	cca Pro	tat Tyr	cgg Arg	gta Val 635	caa Gln	gtg Val	gtg Val	gcc Ala	aca Thr 640	2040

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gaa gta ggg ggg tct tcc ttg agc tct gtg tca gag ttc cac ctg atc Glu Val Gly Gly Ser Ser Leu Ser Ser Val Ser Glu Phe His Leu Ile 645 650 655	2088
ctt atg gat gtg aat gac aac cct ccc agg cta gcc aag gac tac acg Leu Met Asp Val Asn Asp Asn Pro Pro Arg Leu Ala Lys Asp Tyr Thr 660 665 670	2136
ggc ttg ttc ttc tgc cat ccc ctc agt gca cct gga agt ctc att ttc Gly Leu Phe Phe Cys His Pro Leu Ser Ala Pro Gly Ser Leu Ile Phe 675 680 685	2184
gag gct act gat gat gat cag cac tta ttt cgg ggt ccc cat ttt aca Glu Ala Thr Asp Asp Asp Gln His Leu Phe Arg Gly Pro His Phe Thr 690 695 700	2232
ttt tcc ctc ggc agt gga agc tta caa aac gac tgg gaa gtt tcc aaa Phe Ser Leu Gly Ser Gly Ser Leu Gln Asn Asp Trp Glu Val Ser Lys 705 710 715 720	2280
atc aat ggt act cat gcc cga ctg tct acc agg cac aca gag ttt gag Ile Asn Gly Thr His Ala Arg Leu Ser Thr Arg His Thr Glu Phe Glu 725 730 735	2328
gag agg gag tat gtc gtc ttg atc cgc atc aat gat ggg ggt cgg cca Glu Arg Glu Tyr Val Val Leu Ile Arg Ile Asn Asp Gly Gly Arg Pro 740 745 750	2376
ccc ttg gaa ggc att gtt tct tta cca gtt aca ttc tgc agt tgt gtg Pro Leu Glu Gly Ile Val Ser Leu Pro Val Thr Phe Cys Ser Cys Val 755 760 765	2424
gaa gga agt tgt ttc cgg cca gca ggt cac cag act ggg ata ccc act Glu Gly Ser Cys Phe Arg Pro Ala Gly His Gln Thr Gly Ile Pro Thr 770 775 780	2472
gtg ggc atg gca gtt ggt ata ctg ctg acc acc ctt ctg gtg att ggt Val Gly Met Ala Val Gly Ile Leu Leu Thr Thr Leu Leu Val Ile Gly 785 790 795 800	2520
ata att tta gca gtt gtg ttt atc cgc ata aag aag gat aaa ggc aaa Ile Ile Leu Ala Val Val Phe Ile Arg Ile Lys Lys Asp Lys Gly Lys 805 810 815	2568
gat aat gtt gaa agt gct caa gca tct gaa gtc aaa cct ctg aga agc Asp Asn Val Glu Ser Ala Gln Ala Ser Glu Val Lys Pro Leu Arg Ser 820 825 830	2616
tgaatttgaa aaggaatggt tgaatttata tagcaagtgc tatttcagca acaaccatct	2676
catacctatta cttttcatct aacgtgcatt ataatttttt aaacagatat tccctcttgt	2736
cctttaatat ttgctaaata tttctttttt gaggtggagt cttgctctgt cgcccaggct	2796
ggagtacagt ggtgtgatcc cagctcactg caacctccgc ctcttggggtt cacatgattc	2856
tcctgcctca gcttcctaag tagctgggtt tacaggcacc caccacatg cccagctaata	2916
ttttgtatatt ttaatagaga cgggggtttcg ccatttggcc aggctgggtct tgaactcctg	2976
acgtcaagtg atctgcctgc cttgggtctcc caatacaggc atgaaccact gcaccacct	3036
acttagatat ttcattgtgct atagacatta gagagatttt tcatttttcc atgacatttt	3096
tcctctctgc aaatggctta gctacttggtg tttttccctt ttggggcaag acagactcat	3156
taaatattct gtacattttt tctttatcaa ggagatatat cagtgttggtc tcatagaact	3216

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gcctggattc ctttatgtt tttctgatt ccctcctgtg tccccttcat ccttgactcc 3276
tttggtatct cactgaattt caaacatttg tcagagaaga aaaacgtgag gactcaggaa 3336
aaataaataa ataaaagaac agccttttcc cttagtatta acagaaatgt ttctgtgtca 3396
ttaaccatct ttaatcaatg tgacatgttg ctctttggct gaaattcttc aacttggaag 3456
tgacacagac ccacagaagg tgttcaaaca caacctactc tgcaaacctt ggtaaaggaa 3516
ccagtcagct ggccagattt cctcactacc tgccatgcat acatgctgag catgttttct 3576
tcattcgtat gttagtaaag ttttggttat tatatatatta acatgtggaa gaaaacaaga 3636
catgaaaaga gtggtgacaa atcaagaata aacactgggt gtagtcagtt ttgtttgtta 3696
a 3697
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<210> 60
<211> 832
<212> PRT
<213> homo sapiens
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<400> 60
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1 5 10 15
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```
Leu Ala Thr Gly Tyr Gly Gln Glu Gly Lys Phe Ser Gly Pro Leu Lys
20 25 30
```

```
Pro Met Thr Phe Ser Ile Tyr Glu Gly Gln Glu Pro Ser Gln Ile Ile
35 40 45
```

```
Phe Gln Phe Lys Ala Asn Pro Ala Val Thr Phe Glu Leu Thr Gly
50 55 60
```

```
Glu Thr Asp Asn Ile Phe Val Ile Glu Arg Glu Gly Leu Leu Tyr Tyr
65 70 75 80
```

```
Asn Arg Ala Leu Asp Arg Glu Thr Arg Ser Thr His Asn Leu Gln Val
85 90 95
```

```
Ala Ala Leu Asp Ala Asn Gly Ile Ile Val Glu Gly Pro Val Pro Ile
100 105 110
```

```
Thr Ile Glu Val Lys Asp Ile Asn Asp Asn Arg Pro Thr Phe Leu Gln
115 120 125
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Ser Lys Tyr Glu Gly Ser Val Arg Gln Asn Ser Arg Pro Gly Lys Pro
130 135 140
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```
Phe Leu Tyr Val Asn Ala Thr Asp Leu Asp Asp Pro Ala Thr Pro Asn
145 150 155 160
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Gly Gln Leu Tyr Tyr Gln Ile Val Ile Gln Leu Pro Met Ile Asn Asn
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```

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165 170 175

Val Met Tyr Phe Gln Ile Asn Asn Lys Thr Gly Ala Ile Ser Leu Thr  
180 185 190

Arg Glu Gly Ser Gln Glu Leu Asn Pro Ala Lys Asn Pro Ser Tyr Asn  
195 200 205

Leu Val Ile Ser Val Lys Asp Met Gly Gly Gln Ser Glu Asn Ser Phe  
210 215 220

Ser Asp Thr Thr Ser Val Asp Ile Ile Val Thr Glu Asn Ile Trp Lys  
225 230 235 240

Ala Pro Lys Pro Val Glu Met Val Glu Asn Ser Thr Asp Pro His Pro  
245 250 255

Ile Lys Ile Thr Gln Val Arg Trp Asn Asp Pro Gly Ala Gln Tyr Ser  
260 265 270

Leu Val Asp Lys Glu Lys Leu Pro Arg Phe Pro Phe Ser Ile Asp Gln  
275 280 285

Glu Gly Asp Ile Tyr Val Thr Gln Pro Leu Asp Arg Glu Glu Lys Asp  
290 295 300

Ala Tyr Val Phe Tyr Ala Val Ala Lys Asp Glu Tyr Gly Lys Pro Leu  
305 310 315 320

Ser Tyr Pro Leu Glu Ile His Val Lys Val Lys Asp Ile Asn Asp Asn  
325 330 335

Pro Pro Thr Cys Pro Ser Pro Val Thr Val Phe Glu Val Gln Glu Asn  
340 345 350

Glu Arg Leu Gly Asn Ser Ile Gly Thr Leu Thr Ala His Asp Arg Asp  
355 360 365

Glu Glu Asn Thr Ala Asn Ser Phe Leu Asn Tyr Arg Ile Val Glu Gln  
370 375 380

Thr Pro Lys Leu Pro Met Asp Gly Leu Phe Leu Ile Gln Thr Tyr Ala  
385 390 395 400

Gly Met Leu Gln Leu Ala Lys Gln Ser Leu Lys Lys Gln Asp Thr Pro  
405 410 415

Gln Tyr Asn Leu Thr Ile Glu Val Ser Asp Lys Asp Phe Lys Thr Leu  
420 425 430

Cys Phe Val Gln Ile Asn Val Ile Asp Ile Asn Asp Gln Ile Pro Ile



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435

440

445

Phe Glu Lys Ser Asp Tyr Gly Asn Leu Thr Leu Ala Glu Asp Thr Asn  
450 455 460

Ile Gly Ser Thr Ile Leu Thr Ile Gln Ala Thr Asp Ala Asp Glu Pro  
465 470 475 480

Phe Thr Gly Ser Ser Lys Ile Leu Tyr His Ile Ile Lys Gly Asp Ser  
485 490 495

Glu Gly Arg Leu Gly Val Asp Thr Asp Pro His Thr Asn Thr Gly Tyr  
500 505 510

Val Ile Ile Lys Lys Pro Leu Asp Phe Glu Thr Ala Ala Val Ser Asn  
515 520 525

Ile Val Phe Lys Ala Glu Asn Pro Glu Pro Leu Val Phe Gly Val Lys  
530 535 540

Tyr Asn Ala Ser Ser Phe Ala Lys Phe Thr Leu Ile Val Thr Asp Val  
545 550 555 560

Asn Glu Ala Pro Gln Phe Ser Gln His Val Phe Gln Ala Lys Val Ser  
565 570 575

Glu Asp Val Ala Ile Gly Thr Lys Val Gly Asn Val Thr Ala Lys Asp  
580 585 590

Pro Glu Gly Leu Asp Ile Ser Tyr Ser Leu Arg Gly Asp Thr Arg Gly  
595 600 605

Trp Leu Lys Ile Asp His Val Thr Gly Glu Ile Phe Ser Val Ala Pro  
610 615 620

Leu Asp Arg Glu Ala Gly Ser Pro Tyr Arg Val Gln Val Val Ala Thr  
625 630 635 640

Glu Val Gly Gly Ser Ser Leu Ser Ser Val Ser Glu Phe His Leu Ile  
645 650 655

Leu Met Asp Val Asn Asp Asn Pro Pro Arg Leu Ala Lys Asp Tyr Thr  
660 665 670

Gly Leu Phe Phe Cys His Pro Leu Ser Ala Pro Gly Ser Leu Ile Phe  
675 680 685

Glu Ala Thr Asp Asp Asp Gln His Leu Phe Arg Gly Pro His Phe Thr  
690 695 700

Phe Ser Leu Gly Ser Gly Ser Leu Gln Asn Asp Trp Glu Val Ser Lys  
Page 145

705

Ile Asn Gly Thr His Ala Arg Leu Ser Thr Arg His Thr Glu Phe Glu  
725 730 735

Glu Arg Glu Tyr Val Val Leu Ile Arg Ile Asn Asp Gly Gly Arg Pro  
740 745 750

Pro Leu Glu Gly Ile Val Ser Leu Pro Val Thr Phe Cys Ser Cys Val  
755 760 765

Glu Gly Ser Cys Phe Arg Pro Ala Gly His Gln Thr Gly Ile Pro Thr  
770 775 780

Val Gly Met Ala Val Gly Ile Leu Leu Thr Thr Leu Leu Val Ile Gly  
785 790 795 800

Ile Ile Leu Ala Val Val Phe Ile Arg Ile Lys Lys Asp Lys Gly Lys  
805 810 815

Asp Asn Val Glu Ser Ala Gln Ala Ser Glu Val Lys Pro Leu Arg Ser  
820 825 830

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<211> 2920  
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<213> homo sapiens

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<221> CDS  
<222> (10)..(2247)

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Met Ala Trp Ile Arg Ser Thr Cys Ile Leu Phe Phe Thr Leu  
1 5 10

ctt ttt gcc cac ata gca gct gta ccg att aag cat ctt cct gaa gaa 99  
Leu Phe Ala His Ile Ala Ala Val Pro Ile Lys His Leu Pro Glu Glu  
15 20 25 30

aat gta cat gat gca gat ttt ggt gaa cag aag gat att tca gaa atc 147  
Asn Val His Asp Ala Asp Phe Gly Glu Gln Lys Asp Ile Ser Glu Ile  
35 40 45

aat tta gct gca ggc ttg gac ctc ttt caa ggg gac atc ctc ttg cag 195  
Asn Leu Ala Ala Gly Leu Asp Leu Phe Gln Gly Asp Ile Leu Leu Gln  
50 55 60

aaa tcc aga aat ggc ctg aga gac cca aac acc agg tgg acg ttc ccc 243  
Lys Ser Arg Asn Gly Leu Arg Asp Pro Asn Thr Arg Trp Thr Phe Pro  
65 70 75

att cct tac atc ttg gct gat aat ttg ggg ctg aat gct aaa gga gcc 291  
Ile Pro Tyr Ile Leu Ala Asp Asn Leu Gly Leu Asn Ala Lys Gly Ala  
80 85 90

att ctg tat gcc ttt gag atg ttc cgt ctc aag tcc tgt gtg gat ttc 339  
Ile Leu Tyr Ala Phe Glu Met Phe Arg Leu Lys Ser Cys Val Asp Phe  
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95	100	105	110	
aag ccc tat gaa gga gag agc tca tat atc ata ttt caa cag ttt gat	Lys Pro Tyr Glu Gly Glu Ser Ser Tyr Ile Ile Phe Gln Gln Phe Asp			387
ggg tgc tgg tct gag gtt ggt gac caa cat gtg gga cag aac att tcc	Gly Cys Trp Ser Glu Val Gly Asp Gln His Val Gly Gln Asn Ile Ser			435
att ggc caa gga tgt gcc tat aag gcc atc ata gaa cac gag atc ctg	Ile Gly Gln Gly Cys Ala Tyr Lys Ala Ile Ile Glu His Glu Ile Leu			483
cat gct ttg gga ttt tac cac gag cag tca agg acg gac cgg gat gat	His Ala Leu Gly Phe Tyr His Glu Gln Ser Arg Thr Asp Arg Asp Asp			531
tat gtg aac atc tgg tgg gac caa att ctt tca ggt tac cag cac aac	Tyr Val Asn Ile Trp Trp Asp Gln Ile Leu Ser Gly Tyr Gln His Asn			579
ttt gac acc tat gat gat agc tta atc aca gac ctc aat aca ccc tat	Phe Asp Thr Tyr Asp Asp Ser Leu Ile Thr Asp Leu Asn Thr Pro Tyr			627
gat tat gag tct ttg atg cac tac cag cct ttc tca ttt aac aag aat	Asp Tyr Glu Ser Leu Met His Tyr Gln Pro Phe Ser Phe Asn Lys Asn			675
gca agt gtt ccc acc atc aca gcc aag atc cct gag ttt aac tcc att	Ala Ser Val Pro Thr Ile Thr Ala Lys Ile Pro Glu Phe Asn Ser Ile			723
atc gga caa cgc ctg gat ttc agt gcc att gat tta gag agg ctg aac	Ile Gly Gln Arg Leu Asp Phe Ser Ala Ile Asp Leu Glu Arg Leu Asn			771
cga atg tac aat tgc acc aca act cac act ctt ttg gac cac tgt act	Arg Met Tyr Asn Cys Thr Thr Thr His Thr Leu Leu Asp His Cys Thr			819
ttt gag aag gca aac atc tgt gga atg att cag ggc acc aga gat gac	Phe Glu Lys Ala Asn Ile Cys Gly Met Ile Gln Gly Thr Arg Asp Asp			867
act gac tgg gcc cat cag gac agt gct cag gct gga gaa gtg gat cac	Thr Asp Trp Ala His Gln Asp Ser Ala Gln Ala Gly Glu Val Asp His			915
acc ttg ttg gga caa tgc aca ggt gcc ggc tac ttc atg cag ttc agc	Thr Leu Leu Gly Gln Cys Thr Gly Ala Gly Tyr Phe Met Gln Phe Ser			963
acc agc tcg ggg tcc gcg gaa gag gca gcc cta ctg gag tct cgg att	Thr Ser Ser Gly Ser Ala Glu Glu Ala Ala Leu Leu Glu Ser Arg Ile			1011
ctt tac cca aag agg aag cag cag tgc ctg caa ttt ttc tat aaa atg	Leu Tyr Pro Lys Arg Lys Gln Gln Cys Leu Gln Phe Phe Tyr Lys Met			1059
acg gga agt cct tca gac aga ctc gtt gtc tgg gtc agg agg gat gac	Thr Gly Ser Pro Ser Asp Arg Leu Val Val Trp Val Arg Arg Asp Asp			1107
agc aca ggc aat gtt cgc aag ttg gtg aag gtg cag act ttt caa gga	Ser Thr Gly Asn Val Arg Lys Leu Val Lys Val Gln Thr Phe Gln Gly			1155

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370 375 380

gat Asp	gat Asp	gac Asp 385	cac His	aat Asn	tgg Trp	aaa Lys	att Ile 390	gcc Ala	cat His	gtg Val	gtg Val	ctc Leu 395	aaa Lys	gag Glu	gaa Glu	1203
cag Gln	aag Lys 400	ttt Phe	cgc Arg	tac Tyr	ctt Leu	ttc Phe 405	cag Gln	ggc Gly	aca Thr	aaa Lys	ggc Gly 410	gac Asp	cct Pro	cag Gln	aac Asn	1251
tca Ser 415	act Thr	ggg Gly	gga Gly	att Ile	tac Tyr 420	cta Leu	gat Asp	gac Asp	atc Ile	act Thr 425	ctg Leu	aca Thr	gaa Glu	acc Thr	ccc Pro 430	1299
tgc Cys	ccc Pro	aca Thr	ggg Gly	gtc Val 435	tgg Trp	aca Thr	gtc Val	cgg Arg	aat Asn 440	ttc Phe	tcc Ser	caa Gln	gtc Val	ctt Leu 445	gag Glu	1347
aac Asn	acc Thr	agc Ser	aaa Lys 450	ggg Gly	gac Asp	aag Lys	ctt Leu	cag Gln 455	agc Ser	cct Pro	cga Arg	ttc Phe	tac Tyr 460	aat Asn	tcg Ser	1395
gag Glu	gga Gly	tat Tyr 465	ggt Gly	ttt Phe	ggg Gly	gta Val	act Thr 470	tta Leu	tac Tyr	cca Pro	aat Asn	agc Ser 475	aga Arg	gaa Glu	agc Ser	1443
tct Ser	ggt Gly 480	tac Tyr	ttg Leu	aga Arg	ctt Leu	gct Ala 485	ttt Phe	cat His	gtg Val	tgc Cys	agt Ser 490	ggg Gly	gag Glu	aac Asn	gat Asp	1491
gct Ala 495	atc Ile	ctg Leu	gag Glu	tgg Trp	ccg Pro 500	gta Val	gaa Glu	aac Asn	aga Arg	cag Gln 505	gtg Val	ata Ile	att Ile	acc Thr	atc Ile 510	1539
ctt Leu	gac Asp	cag Gln	gag Glu	cct Pro 515	gat Asp	gtc Val	cgg Arg	aac Asn	agg Arg 520	atg Met	tcc Ser	tca Ser	agc Ser	atg Met 525	gtg Val	1587
ttc Phe	act Thr	acc Thr	tcg Ser 530	aag Lys	tcg Ser	cac His	aca Thr	tct Ser 535	cca Pro	gcg Ala	ata Ile	aat Asn	gac Asp 540	act Thr	gtc Val	1635
atc Ile	tgg Trp	gac Asp 545	agg Arg	ccg Pro	tcc Ser	agg Arg	gtg Val 550	gga Gly	acc Thr	tat Tyr	cat His	aca Thr 555	gac Asp	tgt Cys	aat Asn	1683
tgt Cys	ttt Phe 560	aga Arg	agc Ser	atc Ile	gac Asp	ttg Leu 565	ggc Gly	tgg Trp	agt Ser	ggt Gly	ttc Phe 570	att Ile	tcc Ser	cac His	caa Gln	1731
atg Met 575	ctg Leu	aaa Lys	agg Arg	agg Arg	agt Ser 580	ttc Phe	ctg Leu	aaa Lys	aat Asn	gat Asp 585	gac Asp	ctc Leu	atc Ile	ata Ile	ttt Phe 590	1779
gtg Val	gac Asp	ttt Phe	gaa Glu	gat Asp 595	atc Ile	acc Thr	cac His	ctc Leu	agc Ser 600	cag Gln	act Thr	gaa Glu	gtt Val	ccc Pro 605	tct Ser	1827
aaa Lys	ggc Gly	aaa Lys	aga Arg 610	ctg Leu	agc Ser	ccc Pro	caa Gln	ggc Gly 615	ctc Leu	att Ile	ctc Leu	caa Gln 620	ggc Gly	cag Gln	gag Glu	1875
cag Gln	cag Gln	gtc Val 625	tcc Ser	gaa Glu	gaa Glu	ggt Gly	tcg Ser 630	gga Gly	aag Lys	gcc Ala	atg Met	tta Leu 635	gag Glu	gaa Glu	gcc Ala	1923
cta Leu	cct Pro	gtc Val	agc Ser	ctg Leu	agc Ser	cag Gln	ggg Gly	cag Gln	ccc Pro	agc Ser	cga Arg	cag Gln	aag Lys	cgg Arg	tcg Ser	1971

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640	645	650	
gtg gag aac aca ggc ccc ctg gag gac cat aac tgg cca cag tac ttc			2019
Val Glu Asn Thr Gly Pro Leu Glu Asp His Asn Trp Pro Gln Tyr Phe			
655	660	665	670
aga gac cca tgt gac cca aac cct tgc caa aat gac ggc atc tgt gtg			2067
Arg Asp Pro Cys Asp Pro Asn Pro Cys Gln Asn Asp Gly Ile Cys Val			
	675	680	685
aac gtg aag ggg atg gcg agc tgc agg tgc atc tct gga cat gct ttc			2115
Asn Val Lys Gly Met Ala Ser Cys Arg Cys Ile Ser Gly His Ala Phe			
	690	695	700
ttc tac acg ggg gag cgc tgt cag tcg gcc gag gtg cac ggc agt gtc			2163
Phe Tyr Thr Gly Glu Arg Cys Gln Ser Ala Glu Val His Gly Ser Val			
	705	710	715
ctg ggc atg gtg atc gga ggc acg gct ggc gtg atc ttc ttg acc ttc			2211
Leu Gly Met Val Ile Gly Gly Thr Ala Gly Val Ile Phe Leu Thr Phe			
	720	725	730
tcc atc atc gcc atc ctt tcc caa agg cca agg aag tgacctgcct			2257
Ser Ile Ile Ala Ile Leu Ser Gln Arg Pro Arg Lys			
	735	740	745
gctggcattg gccagaccac agcagcacct cctccatgca ggccttaact ttcccatgtt			2317
caatgcagtt tggggcagct tttttatcag ccttgctttg gataggacct ccaaggacta			2377
agcctccagc cccatgtgtg acccttgtca tctctctgcc ccacataatt atgttacttt			2437
gctatgtgct cctaattgtat ctagtgtgtc ctgtgacaac actcatcaca cttcattgta			2497
aatcacttgt tttattgact gtctttccta tagactgtaa gctccatgag ggcaggcaca			2557
tgttgttctc attgaccgtg ctggccccag tgcctagatg catggctggc acattgttgg			2617
cactcaacaa tggttgaatg aataaaacaa taaatgaatg aataactaag atatagaaac			2677
tctcatttat attgcagatt gaatatatat gatgaaattc ttatgttgaa tatgttagaa			2737
tcaaatactc atttttcatt agatacagta gtgtcatcac tcttttaaga tcttgtaaa			2797
gatttcaa at aaaggctact ctggcgagcc aggctgcaca gcatttgctt tcctctgaga			2857
ttctaagaga aggcctttta taaatttaaat aaatattgag ttagcaaaaa aaaaaaaaaa			2917
aaa			2920

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 <211> 746  
 <212> PRT  
 <213> homo sapiens

<400> 62

Met Ala Trp Ile Arg Ser Thr Cys Ile Leu Phe Phe Thr Leu Leu Phe  
 1 5 10 15

Ala His Ile Ala Ala Val Pro Ile Lys His Leu Pro Glu Glu Asn Val  
 20 25 30

His Asp Ala Asp Phe Gly Glu Gln Lys Asp Ile Ser Glu Ile Asn Leu  
 35 40 45

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Ala Ala Gly Leu Asp Leu Phe Gln Gly Asp Ile Leu Leu Gln Lys Ser  
50 55 60

Arg Asn Gly Leu Arg Asp Pro Asn Thr Arg Trp Thr Phe Pro Ile Pro  
65 70 75 80

Tyr Ile Leu Ala Asp Asn Leu Gly Leu Asn Ala Lys Gly Ala Ile Leu  
85 90 95

Tyr Ala Phe Glu Met Phe Arg Leu Lys Ser Cys Val Asp Phe Lys Pro  
100 105 110

Tyr Glu Gly Glu Ser Ser Tyr Ile Ile Phe Gln Gln Phe Asp Gly Cys  
115 120 125

Trp Ser Glu Val Gly Asp Gln His Val Gly Gln Asn Ile Ser Ile Gly  
130 135 140

Gln Gly Cys Ala Tyr Lys Ala Ile Ile Glu His Glu Ile Leu His Ala  
145 150 155 160

Leu Gly Phe Tyr His Glu Gln Ser Arg Thr Asp Arg Asp Asp Tyr Val  
165 170 175

Asn Ile Trp Trp Asp Gln Ile Leu Ser Gly Tyr Gln His Asn Phe Asp  
180 185 190

Thr Tyr Asp Asp Ser Leu Ile Thr Asp Leu Asn Thr Pro Tyr Asp Tyr  
195 200 205

Glu Ser Leu Met His Tyr Gln Pro Phe Ser Phe Asn Lys Asn Ala Ser  
210 215 220

Val Pro Thr Ile Thr Ala Lys Ile Pro Glu Phe Asn Ser Ile Ile Gly  
225 230 235 240

Gln Arg Leu Asp Phe Ser Ala Ile Asp Leu Glu Arg Leu Asn Arg Met  
245 250 255

Tyr Asn Cys Thr Thr Thr His Thr Leu Leu Asp His Cys Thr Phe Glu  
260 265 270

Lys Ala Asn Ile Cys Gly Met Ile Gln Gly Thr Arg Asp Asp Thr Asp  
275 280 285

Trp Ala His Gln Asp Ser Ala Gln Ala Gly Glu Val Asp His Thr Leu  
290 295 300

Leu Gly Gln Cys Thr Gly Ala Gly Tyr Phe Met Gln Phe Ser Thr Ser  
305 310 315 320

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Ser Gly Ser Ala Glu Glu Ala Ala Leu Leu Glu Ser Arg Ile Leu Tyr  
325 330 335

Pro Lys Arg Lys Gln Gln Cys Leu Gln Phe Phe Tyr Lys Met Thr Gly  
340 345 350

Ser Pro Ser Asp Arg Leu Val Val Trp Val Arg Arg Asp Asp Ser Thr  
355 360 365

Gly Asn Val Arg Lys Leu Val Lys Val Gln Thr Phe Gln Gly Asp Asp  
370 375 380

Asp His Asn Trp Lys Ile Ala His Val Val Leu Lys Glu Glu Gln Lys  
385 390 395 400

Phe Arg Tyr Leu Phe Gln Gly Thr Lys Gly Asp Pro Gln Asn Ser Thr  
405 410 415

Gly Gly Ile Tyr Leu Asp Asp Ile Thr Leu Thr Glu Thr Pro Cys Pro  
420 425 430

Thr Gly Val Trp Thr Val Arg Asn Phe Ser Gln Val Leu Glu Asn Thr  
435 440 445

Ser Lys Gly Asp Lys Leu Gln Ser Pro Arg Phe Tyr Asn Ser Glu Gly  
450 455 460

Tyr Gly Phe Gly Val Thr Leu Tyr Pro Asn Ser Arg Glu Ser Ser Gly  
465 470 475 480

Tyr Leu Arg Leu Ala Phe His Val Cys Ser Gly Glu Asn Asp Ala Ile  
485 490 495

Leu Glu Trp Pro Val Glu Asn Arg Gln Val Ile Ile Thr Ile Leu Asp  
500 505 510

Gln Glu Pro Asp Val Arg Asn Arg Met Ser Ser Ser Met Val Phe Thr  
515 520 525

Thr Ser Lys Ser His Thr Ser Pro Ala Ile Asn Asp Thr Val Ile Trp  
530 535 540

Asp Arg Pro Ser Arg Val Gly Thr Tyr His Thr Asp Cys Asn Cys Phe  
545 550 555 560

Arg Ser Ile Asp Leu Gly Trp Ser Gly Phe Ile Ser His Gln Met Leu  
565 570 575

Lys Arg Arg Ser Phe Leu Lys Asn Asp Asp Leu Ile Ile Phe Val Asp  
580 585 590

122257 sequence listing May 10 2006.ST25.txt

Phe Glu Asp Ile Thr His Leu Ser Gln Thr Glu Val Pro Ser Lys Gly  
595 600 605

Lys Arg Leu Ser Pro Gln Gly Leu Ile Leu Gln Gly Gln Glu Gln Gln  
610 615 620

Val Ser Glu Glu Gly Ser Gly Lys Ala Met Leu Glu Glu Ala Leu Pro  
625 630 635 640

Val Ser Leu Ser Gln Gly Gln Pro Ser Arg Gln Lys Arg Ser Val Glu  
645 650 655

Asn Thr Gly Pro Leu Glu Asp His Asn Trp Pro Gln Tyr Phe Arg Asp  
660 665 670

Pro Cys Asp Pro Asn Pro Cys Gln Asn Asp Gly Ile Cys Val Asn Val  
675 680 685

Lys Gly Met Ala Ser Cys Arg Cys Ile Ser Gly His Ala Phe Phe Tyr  
690 695 700

Thr Gly Glu Arg Cys Gln Ser Ala Glu Val His Gly Ser Val Leu Gly  
705 710 715 720

Met Val Ile Gly Gly Thr Ala Gly Val Ile Phe Leu Thr Phe Ser Ile  
725 730 735

Ile Ala Ile Leu Ser Gln Arg Pro Arg Lys  
740 745

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<212> DNA  
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<220>  
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Met Thr Ser Ile His Phe Val  
1 5

gtt cac ccg ctg ccg ggc acc gag gac cag ctc aat gac agg tta cga 102  
Val His Pro Leu Pro Gly Thr Glu Asp Gln Leu Asn Asp Arg Leu Arg  
10 15 20

gaa gtt tct gag aag ctg aac aaa tat aat tta aac agc cac ccc cct 150  
Glu Val Ser Glu Lys Leu Asn Lys Tyr Asn Leu Asn Ser His Pro Pro  
25 30 35

ttg aat gta ttg gaa cag gct act att aaa cag tgt gtg gtg gga cca 198  
Leu Asn Val Leu Glu Gln Ala Thr Ile Lys Gln Cys Val Val Gly Pro  
40 45 50 55



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aat cat gct gcc ttt ctt ctt gag gat ggt aga gtt tgc agg att ggt	246
Asn His Ala Ala Phe Leu Leu Glu Asp Gly Arg Val Cys Arg Ile Gly	
	60
ttt tca gta cag cca gac aga ttg gaa ttg ggt aaa cct gat aat aat	294
Phe Ser Val Gln Pro Asp Arg Leu Glu Leu Gly Lys Pro Asp Asn Asn	
	75
gat ggg tca aag ttg aac agc aac tcg ggg gca ggg agg acg tca agg	342
Asp Gly Ser Lys Leu Asn Ser Asn Ser Gly Ala Gly Arg Thr Ser Arg	
	90
cct ggt agg aca agc gac tct cca tgg ttt ctc tca ggt tct gag act	390
Pro Gly Arg Thr Ser Asp Ser Pro Trp Phe Leu Ser Gly Ser Glu Thr	
	105
cta ggc agg ctg gca ggc aac acc tta gga agc ser cgc tgg agt tct gga	438
Leu Gly Arg Leu Ala Gly Asn Thr Leu Gly Ser Arg Trp Ser Ser Gly	
	120
gtg ggt gga agt ggt gga gga tcc tct ggt agg tca tca gct gga gct	486
Val Gly Gly Ser Gly Gly Gly Ser Ser Gly Arg Ser Ser Ala Gly Ala	
	140
cga gat tcc cgc cgg cag act cga gtt att cgg aca gga cgg gat cga	534
Arg Asp Ser Arg Arg Gln Thr Arg Val Ile Arg Thr Gly Arg Asp Arg	
	155
ggg tct ggg ctt ttg ggc agt cag ccc cag cca gtt att cca gca tct	582
Gly Ser Gly Leu Leu Gly Ser Gln Pro Gln Pro Val Ile Pro Ala Ser	
	170
gtc att cca gag gag ctg att tca cag gcc caa gtt gtt tta caa ggc	630
Val Ile Pro Glu Glu Leu Ile Ser Gln Ala Gln Val Val Leu Gln Gly	
	185
aaa tcc aga agt gtc att att cga gaa ctt cag aga aca aat ctt gat	678
Lys Ser Arg Ser Val Ile Ile Arg Glu Leu Gln Arg Thr Asn Leu Asp	
	200
gtg aac ctt gct gta aat aat tta ctt agc cgg gat gat gaa gat gga	726
Val Asn Leu Ala Val Asn Asn Leu Leu Ser Arg Asp Asp Glu Asp Gly	
	220
gat gat ggg gat gat aca gcc agc gaa tct tat ttg cct gga gag gat	774
Asp Asp Gly Asp Asp Thr Ala Ser Glu Ser Tyr Leu Pro Gly Glu Asp	
	235
ctt atg tct ctc ctt gat gcc gac att cat tct gcc cac cca agt gtc	822
Leu Met Ser Leu Leu Asp Ala Asp Ile His Ser Ala His Pro Ser Val	
	250
att att gat gca gat gcc atg ttt tct gaa gac att agc tat ttt ggt	870
Ile Ile Asp Ala Asp Ala Met Phe Ser Glu Asp Ile Ser Tyr Phe Gly	
	265
tac cct tct ttt cgt cgt tca tca ctt tcc agg cta ggc tca tct cga	918
Tyr Pro Ser Phe Arg Arg Ser Ser Leu Ser Arg Leu Gly Ser Ser Arg	
	280
gtt ctc ctt ctt ccc tta gag aga gac tct gag ctg ttg cgt gaa cgt	966
Val Leu Leu Leu Pro Leu Glu Arg Asp Ser Glu Leu Leu Arg Glu Arg	
	300
gaa tcc gtt tta cgt tta cgt gaa cga agg tgg ctt gat gga gcc tca	1014
Glu Ser Val Leu Arg Leu Arg Glu Arg Arg Trp Leu Asp Gly Ala Ser	
	315

## 122257 sequence listing May 10 2006.ST25.txt

ttt gat aat gaa agg ggt tct acc agc aag gaa gga gag cca aac ttg	1062
Phe Asp Asn Glu Arg Gly Ser Thr Ser Lys Glu Gly Glu Pro Asn Leu	
330	
335	
340	
gat aag aag aat aca cct gtt caa agt cca gta tct cta gga gaa gat	1110
Asp Lys Lys Asn Thr Pro Val Gln Ser Pro Val Ser Leu Gly Glu Asp	
345	
350	
355	
ttg cag tgg tgg cct gat aag gat gga aca aaa ttc atc tgt att ggg	1158
Leu Gln Trp Trp Pro Asp Lys Asp Gly Thr Lys Phe Ile Cys Ile Gly	
360	
365	
370	
375	
gct ctg tat tct gaa ctt ctg gct gtc agc agt aaa gga gaa ctt tat	1206
Ala Leu Tyr Ser Glu Leu Leu Ala Val Ser Lys Gly Glu Leu Tyr	
380	
385	
390	
cag tgg aaa tgg agt gaa tct gag cct tac aga aat gcc cag aat cct	1254
Gln Trp Lys Trp Ser Glu Ser Glu Pro Tyr Arg Asn Ala Gln Asn Pro	
395	
400	
405	
tca tta cat cat cca cga gca aca ttt ttg ggg tta acc aat gaa aag	1302
Ser Leu His His Pro Arg Ala Thr Phe Leu Gly Leu Thr Asn Glu Lys	
410	
415	
420	
ata gtc ctc ctg tct gca aat agc ata aga gca act gta gct aca gaa	1350
Ile Val Leu Leu Ser Ala Asn Ser Ile Arg Ala Thr Val Ala Thr Glu	
425	
430	
435	
aat aac aag gtt gct aca tgg gtg gat gaa act tta agt tct gtg gct	1398
Asn Asn Lys Val Ala Thr Trp Val Asp Glu Thr Leu Ser Ser Val Ala	
440	
445	
450	
455	
tct aaa tta gag cac act gct cag act tac tct gaa ctt caa gga gag	1446
Ser Lys Leu Glu His Thr Ala Gln Thr Tyr Ser Glu Leu Gln Gly Glu	
460	
465	
470	
cgg ata gtt tct tta cat tgc tgt gcc ctt tac acc tgc gct cag ctg	1494
Arg Ile Val Ser Leu His Cys Cys Ala Leu Tyr Thr Cys Ala Gln Leu	
475	
480	
485	
gaa aac agt tta tat tgg tgg ggt gta gtt cct ttt agt caa agg aag	1542
Glu Asn Ser Leu Tyr Trp Trp Gly Val Val Pro Phe Ser Gln Arg Lys	
490	
495	
500	
aaa atg tta gag aaa gct aga gca aaa aat aaa aag cct aaa tcc agt	1590
Lys Met Leu Glu Lys Ala Arg Ala Lys Asn Lys Lys Pro Lys Ser Ser	
505	
510	
515	
gct ggt att tct tca atg ccg aac atc act gtt ggt acc cag gta tgc	1638
Ala Gly Ile Ser Ser Met Pro Asn Ile Thr Val Gly Thr Gln Val Cys	
520	
525	
530	
535	
ttg aga aat aat cct ctt tat cat gct gga gca gtt gca ttt tca att	1686
Leu Arg Asn Asn Pro Leu Tyr His Ala Gly Ala Val Ala Phe Ser Ile	
540	
545	
550	
agt gct ggg att cct aaa gtt ggt gtc tta atg gag tca gtt tgg aat	1734
Ser Ala Gly Ile Pro Lys Val Gly Val Leu Met Glu Ser Val Trp Asn	
555	
560	
565	
atg aat gac agc tgt aga ttt caa ctt aga tct cct gaa agc ttg aaa	1782
Met Asn Asp Ser Cys Arg Phe Gln Leu Arg Ser Pro Glu Ser Leu Lys	
570	
575	
580	
aac atg gaa aaa gct agc aaa act act gaa gct aag cct gaa agt aag	1830
Asn Met Glu Lys Ala Ser Lys Thr Thr Glu Ala Lys Pro Glu Ser Lys	
585	
590	
595	

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cag Gln 600	gag Glu	cca Pro	gtg Val	aaa Lys	aca Thr 605	gaa Glu	atg Met	ggt Gly	cct Pro	cca Pro 610	cca Pro	tct Ser	cca Pro	gca Ala	tcc Ser 615	1878
acg Thr	tgt Cys	agt Ser	gat Asp	gca Ala 620	tcc Ser	tca Ser	att Ile	gcc Ala	agc Ser 625	agt Ser	gca Ala	tca Ser	atg Met	cca Pro 630	tac Tyr	1926
aaa Lys	cga Arg	cga Arg	cgg Arg 635	tca Ser	acc Thr	cct Pro	gca Ala	cca Pro 640	aaa Lys	gaa Glu	gag Glu	gaa Glu	aag Lys 645	gtg Val	aat Asn	1974
gaa Glu	gag Glu	cag Gln 650	tgg Trp	tct Ser	ctt Leu	cgg Arg	gaa Glu 655	gtg Val	gtt Val	ttt Phe	gtg Val	gaa Glu 660	gat Asp	gtc Val	aag Lys	2022
aat Asn 665	gtt Val	cct Pro	gtt Val	ggc Gly	aag Lys	gtg Val 670	cta Leu	aaa Lys	gta Val	gat Asp	ggt Gly 675	gcc Ala	tat Tyr	gtt Val	gct Ala	2070
gta Val 680	aaa Lys	ttt Phe	cca Pro	gga Gly	acc Thr 685	tcc Ser	agt Ser	aat Asn	act Thr	aac Asn 690	tgt Cys	cag Gln	aac Asn	agc Ser	tct Ser 695	2118
ggt Gly	cca Pro	gat Asp	gct Ala	gac Asp 700	cct Pro	tct Ser	tct Ser	ctc Leu	ctg Leu 705	cag Gln	gat Asp	tgt Cys	agg Arg	tta Leu 710	ctt Leu	2166
aga Arg	att Ile	gat Asp	gaa Glu 715	ttg Leu	cag Gln	gtt Val	gtc Val	aaa Lys 720	act Thr	ggt Gly	gga Gly	aca Thr	ccg Pro 725	aag Lys	gtt Val	2214
ccc Pro	gac Asp	tgt Cys 730	ttc Phe	caa Gln	agg Arg	act Thr	cct Pro 735	aaa Lys	aag Lys	ctt Leu	tgt Cys	ata Ile 740	cct Pro	gaa Glu	aaa Lys	2262
aca Thr 745	gaa Glu	ata Ile	tta Leu	gca Ala	gtg Val	aat Asn 750	gta Val	gat Asp	tcc Ser	aaa Lys 755	ggt Gly	gtt Val	cat His	gct Ala	gtt Val	2310
ctg Leu 760	aag Lys	act Thr	gga Gly	aat Asn	tgg Trp 765	gtg Val	cga Arg	tac Tyr	tgt Cys	atc Ile 770	ttt Phe	gat Asp	ctt Leu	gct Ala	aca Thr 775	2358
gga Gly	aaa Lys	gca Ala	gaa Glu	cag Gln 780	gaa Glu	aat Asn	aat Asn	ttt Phe	cct Pro 785	aca Thr	agc Ser	agc Ser	att Ile	gct Ala 790	ttc Phe	2406
ctt Leu	ggt Gly	cag Gln	aat Asn 795	gag Glu	agg Arg	aat Asn	gta Val	gcc Ala 800	att Ile	ttc Phe	act Thr	gct Ala	gga Gly 805	cag Gln	gaa Glu	2454
tct Ser	ccc Pro	att Ile 810	att Ile	ctt Leu	cga Arg	gat Asp	gga Gly 815	aat Asn	ggt Gly	acc Thr	atc Ile	tac Tyr 820	cca Pro	atg Met	gcc Ala	2502
aaa Lys	gat Asp 825	tgc Cys	atg Met	gga Gly	gga Gly	ata Ile 830	agg Arg	gat Asp	ccc Pro	gat Asp	tgg Trp 835	ctg Leu	gat Asp	ctt Leu	cca Pro	2550
cct Pro 840	att Ile	agt Ser	agt Ser	ctt Leu	gga Gly 845	atg Met	ggt Gly	gtg Val	cat His 850	tct Ser	tta Leu	ata Ile	aat Asn	ctt Leu	cct Pro 855	2598
gcc Ala	aat Asn	tca Ser	aca Thr	atc Ile 860	aaa Lys	aag Lys	aaa Lys	gct Ala	gct Ala 865	gtt Val	atc Ile	atc Ile	atg Met	gct Ala 870	gta Val	2646

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gag	aaa	caa	acc	tta	atg	caa	cac	att	ctg	cgc	tgt	gac	tat	gag	gcc	2694
Glu	Lys	Gln	Thr	Leu	Met	Gln	His	Ile	Leu	Arg	Cys	Asp	Tyr	Glu	Ala	
			875					880					885			
tgt	cga	caa	tat	cta	atg	aat	ctt	gag	caa	gcg	gtt	gtt	tta	gag	cag	2742
Cys	Arg	Gln	Tyr	Leu	Met	Asn	Leu	Glu	Gln	Ala	Val	Val	Leu	Glu	Gln	
		890					895					900				
aat	cta	cag	atg	ctg	cag	aca	ttc	atc	agc	cac	aga	tgt	gat	gga	aat	2790
Asn	Leu	Gln	Met	Leu	Gln	Thr	Phe	Ile	Ser	His	Arg	Cys	Asp	Gly	Asn	
	905					910					915					
cga	aat	att	ttg	cat	gct	tgt	gta	tca	gtt	tgc	ttt	cca	acc	agc	aat	2838
Arg	Asn	Ile	Leu	His	Ala	Cys	Val	Ser	Val	Cys	Phe	Pro	Thr	Ser	Asn	
920					925					930					935	
aaa	gaa	act	aaa	gaa	gaa	gag	gaa	gcg	gag	cgt	tct	gaa	aga	aat	aca	2886
Lys	Glu	Thr	Lys	Glu	Glu	Glu	Glu	Ala	Glu	Arg	Ser	Glu	Arg	Asn	Thr	
				940					945					950		
ttt	gca	gaa	agg	ctt	tct	gct	gtt	gag	gcc	att	gca	aat	gca	ata	tca	2934
Phe	Ala	Glu	Arg	Leu	Ser	Ala	Val	Glu	Ala	Ile	Ala	Asn	Ala	Ile	Ser	
			955					960					965			
gtt	gtt	tca	agt	aat	ggc	cca	ggt	aat	cgg	gct	gga	tca	tca	agt	agc	2982
Val	Val	Ser	Ser	Asn	Gly	Pro	Gly	Asn	Arg	Ala	Gly	Ser	Ser	Ser	Ser	
		970					975					980				
cga	agt	ttg	aga	tta	cgg	gaa	atg	atg	aga	cgt	tcg	ttg	aga	gca	gct	3030
Arg	Ser	Leu	Arg	Leu	Arg	Glu	Met	Met	Arg	Arg	Ser	Leu	Arg	Ala	Ala	
	985					990					995					
ggt	ttg	ggt	aga	cat	gaa	gct	gga	gct	tca	tcc	agt	gac	cac	cag		3075
Gly	Leu	Gly	Arg	His	Glu	Ala	Gly	Ala	Ser	Ser	Ser	Asp	His	Gln		
1000					1005					1010						
gat	cca	gtt	tca	ccc	ccc	ata	gct	ccc	cct	agt	tgg	gtt	cct	gac		3120
Asp	Pro	Val	Ser	Pro	Pro	Ile	Ala	Pro	Pro	Ser	Trp	Val	Pro	Asp		
1015					1020					1025						
cct	cct	gcg	atg	gat	cct	gat	ggt	gac	att	gat	ttt	atc	ctg	gcc		3165
Pro	Pro	Ala	Met	Asp	Pro	Asp	Gly	Asp	Ile	Asp	Phe	Ile	Leu	Ala		
1030					1035					1040						
ccc	gct	gtg	gga	tct	ctt	acc	aca	gca	gca	acc	ggt	act	ggt	caa		3210
Pro	Ala	Val	Gly	Ser	Leu	Thr	Thr	Ala	Ala	Thr	Gly	Thr	Gly	Gln		
1045					1050					1055						
gga	cca	agc	acc	tcc	act	att	cca	ggt	cct	tcc	aca	gag	cca	tct		3255
Gly	Pro	Ser	Thr	Ser	Thr	Ile	Pro	Gly	Pro	Ser	Thr	Glu	Pro	Ser		
1060					1065					1070						
gta	gta	gaa	tcc	aag	gat	cga	aag	gcg	aat	gct	cat	ttt	ata	ttg		3300
Val	Val	Glu	Ser	Lys	Asp	Arg	Lys	Ala	Asn	Ala	His	Phe	Ile	Leu		
1075					1080					1085						
aaa	ttg	tta	tgt	gac	agt	gtg	gtt	ctc	cag	ccc	tat	cta	cga	gaa		3345
Lys	Leu	Leu	Cys	Asp	Ser	Val	Val	Leu	Gln	Pro	Tyr	Leu	Arg	Glu		
1090					1095					1100						
ctt	ctt	tct	gcc	aag	gat	gca	aga	ggg	atg	acc	cca	ttt	atg	tca		3390
Leu	Leu	Ser	Ala	Lys	Asp	Ala	Arg	Gly	Met	Thr	Pro	Phe	Met	Ser		
1105					1110					1115						
gct	gta	agt	ggc	cga	gct	tat	cct	gct	gca	att	acc	atc	tta	gaa		3435
Ala	Val	Ser	Gly	Arg	Ala	Tyr	Pro	Ala	Ala	Ile	Thr	Ile	Leu	Glu		
1120					1125					1130						

## 122257 sequence listing May 10 2006.ST25.txt

act Thr 1135	gct Ala	cag Gln	aaa Lys	att Ile	gca Ala 1140	aaa Lys	gct Ala	gaa Glu	ata Ile	tcc Ser 1145	tca Ser	agt Ser	gaa Glu	aaa Lys	3480
gag Glu 1150	gaa Glu	gat Asp	gta Val	ttc Phe	atg Met 1155	gga Gly	atg Met	gtt Val	tgc Cys	cca Pro 1160	tca Ser	ggt Gly	acc Thr	aac Asn	3525
cct Pro 1165	gat Asp	gac Asp	tct Ser	cct Pro	tta Leu 1170	tat Tyr	gtt Val	tta Leu	tgt Cys	tgt Cys 1175	aat Asn	gac Asp	act Thr	tgc Cys	3570
agt Ser 1180	ttt Phe	aca Thr	tgg Trp	act Thr	gga Gly 1185	gca Ala	gag Glu	cac His	att Ile	aac Asn 1190	cag Gln	gat Asp	att Ile	ttt Phe	3615
gag Glu 1195	tgt Cys	cga Arg	act Thr	tgt Cys	ggc Gly 1200	ttg Leu	ctg Leu	gag Glu	tca Ser	ctg Leu 1205	tgt Cys	tgt Cys	tgt Cys	acg Thr	3660
gaa Glu 1210	tgt Cys	gca Ala	agg Arg	gtt Val	tgt Cys 1215	cat His	aaa Lys	ggt Gly	cat His	gat Asp 1220	tgc Cys	aaa Lys	ctc Leu	aaa Lys	3705
cgg Arg 1225	aca Thr	tca Ser	cca Pro	aca Thr	gcc Ala 1230	tac Tyr	tgt Cys	gat Asp	tgt Cys	tgg Trp 1235	gag Glu	aaa Lys	tgt Cys	aaa Lys	3750
tgt Cys 1240	aaa Lys	act Thr	ctt Leu	att Ile	gct Ala 1245	gga Gly	cag Gln	aaa Lys	tct Ser	gct Ala 1250	cgt Arg	ctt Leu	gat Asp	cta Leu	3795
ctt Leu 1255	tat Tyr	cgc Arg	ctg Leu	ctc Leu	act Thr 1260	gct Ala	act Thr	aat Asn	ctg Leu	gtt Val 1265	act Thr	ctg Leu	cca Pro	aac Asn	3840
agc Ser 1270	agg Arg	gga Gly	gag Glu	cac His	ctc Leu 1275	tta Leu	cta Leu	ttc Phe	tta Leu	gta Val 1280	cag Gln	aca Thr	gtc Val	gca Ala	3885
agg Arg 1285	cag Gln	acg Thr	gtg Val	gag Glu	cat His 1290	tgt Cys	caa Gln	tac Tyr	agg Arg	cca Pro 1295	cct Pro	cga Arg	atc Ile	agg Arg	3930
gaa Glu 1300	gat Asp	cgt Arg	aac Asn	cga Arg	aaa Lys 1305	aca Thr	gcc Ala	agt Ser	cct Pro	gaa Glu 1310	gat Asp	tca Ser	gat Asp	atg Met	3975
cca Pro 1315	gat Asp	cat His	gat Asp	tta Leu	gag Glu 1320	cct Pro	cca Pro	aga Arg	ttt Phe	gcc Ala 1325	cag Gln	ctt Leu	gca Ala	ttg Leu	4020
gag Glu 1330	cgt Arg	gtt Val	cta Leu	cag Gln	gac Asp 1335	tgg Trp	aat Asn	gcc Ala	ttg Leu	aaa Lys 1340	tct Ser	atg Met	att Ile	atg Met	4065
ttt Phe 1345	ggg Gly	tcg Ser	cag Gln	gag Glu	aat Asn 1350	aaa Lys	gac Asp	cct Pro	ctt Leu	agt Ser 1355	gcc Ala	agc Ser	agt Ser	aga Arg	4110
ata Ile 1360	ggc Gly	cat His	ctt Leu	ttg Leu	cca Pro 1365	gaa Glu	gag Glu	caa Gln	gta Val	tac Tyr 1370	ctc Leu	aat Asn	cag Gln	caa Gln	4155
agt Ser 1375	ggc Gly	aca Thr	att Ile	cgg Arg	ctg Leu 1380	gac Asp	tgt Cys	ttc Phe	act Thr	cat His 1385	tgc Cys	ctt Leu	ata Ile	gtt Val	4200

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aag Lys 1390	tgt Cys	aca Thr	gca Ala	gat Asp	att Ile 1395	ttg Leu	ctt Leu	tta Leu	gat Asp	act Thr 1400	cta Leu	cta Leu	ggt Gly	aca Thr	4245
cta Leu 1405	gtg Val	aaa Lys	gaa Glu	ctc Leu	caa Gln 1410	aac Asn	aaa Lys	tat Tyr	aca Thr	cct Pro 1415	gga Gly	cgt Arg	aga Arg	gaa Glu	4290
gaa Glu 1420	gct Ala	att Ile	gct Ala	gtg Val	aca Thr 1425	atg Met	agg Arg	ttt Phe	cta Leu	cgt Arg 1430	tca Ser	gtg Val	gca Ala	aga Arg	4335
gtt Val 1435	ttt Phe	gtt Val	att Ile	ctg Leu	agt Ser 1440	gtg Val	gaa Glu	atg Met	gct Ala	tca Ser 1445	tcc Ser	aaa Lys	aag Lys	aaa Lys	4380
aac Asn 1450	aac Asn	ttt Phe	att Ile	cca Pro	cag Gln 1455	cca Pro	att Ile	gga Gly	aaa Lys	tgc Cys 1460	aag Lys	cgt Arg	gta Val	ttc Phe	4425
caa Gln 1465	gca Ala	ttg Leu	cta Leu	cct Pro	tac Tyr 1470	gct Ala	gtg Val	gaa Glu	gaa Glu	ttg Leu 1475	tgc Cys	aac Asn	gta Val	gca Ala	4470
gag Glu 1480	tca Ser	ctg Leu	att Ile	gtt Val	cct Pro 1485	gtc Val	aga Arg	atg Met	ggg Gly	att Ile 1490	gct Ala	cgt Arg	cca Pro	act Thr	4515
gca Ala 1495	cca Pro	ttt Phe	acc Thr	ctg Leu	gct Ala 1500	agt Ser	act Thr	agc Ser	ata Ile	gat Asp 1505	gcc Ala	atg Met	cag Gln	ggc Gly	4560
agt Ser 1510	gaa Glu	gaa Glu	tta Leu	ttt Phe	tca Ser 1515	gtg Val	gaa Glu	cca Pro	cta Leu	cca Pro 1520	cca Pro	cga Arg	cca Pro	tca Ser	4605
tct Ser 1525	gat Asp	cag Gln	tct Ser	agc Ser	agc Ser 1530	tcc Ser	agt Ser	cag Gln	tct Ser	cag Gln 1535	tca Ser	tcc Ser	tac Tyr	atc Ile	4650
atc Ile 1540	agg Arg	aat Asn	cca Pro	cag Gln	cag Gln 1545	agg Arg	cgc Arg	atc Ile	agc Ser	cag Gln 1550	tca Ser	cag Gln	ccc Pro	gtt Val	4695
cgg Arg 1555	ggc Gly	aga Arg	gat Asp	gaa Glu	gaa Glu 1560	cag Gln	gat Asp	gat Asp	att Ile	gtt Val 1565	tca Ser	gca Ala	gat Asp	gtg Val	4740
gaa Glu 1570	gag Glu	gtt Val	gag Glu	gtg Val	gtg Val 1575	gag Glu	ggt Gly	gtg Val	gct Ala	gga Gly 1580	gaa Glu	gag Glu	gat Asp	cat His	4785
cat His 1585	gat Asp	gaa Glu	cag Gln	gaa Glu	gaa Glu 1590	cac His	ggg Gly	gaa Glu	gaa Glu	aat Asn 1595	gct Ala	gag Glu	gca Ala	gag Glu	4830
gga Gly 1600	caa Gln	cat His	gat Asp	gag Glu	cat His 1605	gat Asp	gaa Glu	gac Asp	ggg Gly	agt Ser 1610	gat Asp	atg Met	gag Glu	ctg Leu	4875
gac Asp 1615	ttg Leu	tta Leu	gca Ala	gca Ala	gct Ala 1620	gaa Glu	aca Thr	gaa Glu	agt Ser	gat Asp 1625	agt Ser	gaa Glu	agt Ser	aac Asn	4920
cac His 1630	agc Ser	aac Asn	caa Gln	gat Asp	aat Asn 1635	gct Ala	agt Ser	ggg Gly	cgc Arg	aga Arg 1640	agc Ser	gtt Val	gtc Val	act Thr	4965

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gca Ala 1645	gca Ala	act Thr	gct Ala	ggt Gly	tca Ser 1650	gaa Glu	gca Ala	gga Gly	gca Ala	agc Ser 1655	agt Ser	gtt Val	cct Pro	gcc Ala	5010
ttc Phe 1660	ttt Phe	tct Ser	gaa Glu	gat Asp	gat Asp 1665	tct Ser	caa Gln	tcg Ser	aat Asn	gac Asp 1670	tca Ser	agt Ser	gat Asp	tct Ser	5055
gat Asp 1675	agc Ser	agt Ser	agt Ser	agt Ser	cag Gln 1680	agt Ser	gac Asp	gac Asp	ata Ile	gaa Glu 1685	cag Gln	gag Glu	acc Thr	ttt Phe	5100
atg Met 1690	ctt Leu	gat Asp	gag Glu	cca Pro	tta Leu 1695	gaa Glu	aga Arg	acc Thr	aca Thr	aat Asn 1700	agc Ser	tcc Ser	cat His	gcc Ala	5145
aat Asn 1705	ggt Gly	gct Ala	gcc Ala	caa Gln	gct Ala 1710	ccc Pro	cgt Arg	tca Ser	atg Met	cag Gln 1715	tgg Trp	gct Ala	gtc Val	cgc Arg	5190
aac Asn 1720	acc Thr	cag Gln	cat His	cag Gln	cga Arg 1725	gca Ala	gcc Ala	agt Ser	aca Thr	gcc Ala 1730	cct Pro	tcc Ser	agt Ser	aca Thr	5235
tct Ser 1735	aca Thr	cca Pro	gca Ala	gca Ala	agt Ser 1740	tca Ser	gcg Ala	ggt Gly	ttg Leu	att Ile 1745	tat Tyr	att Ile	gat Asp	cct Pro	5280
tca Ser 1750	aac Asn	tta Leu	cgc Arg	cgg Arg	agt Ser 1755	ggt Gly	acc Thr	atc Ile	agt Ser	aca Thr 1760	agt Ser	gct Ala	gca Ala	gct Ala	5325
gca Ala 1765	gca Ala	gct Ala	gct Ala	ttg Leu	gaa Glu 1770	gct Ala	agc Ser	aac Asn	gcc Ala	agc Ser 1775	agt Ser	tac Tyr	cta Leu	aca Thr	5370
tct Ser 1780	gca Ala	agc Ser	agt Ser	tta Leu	gcc Ala 1785	agg Arg	gct Ala	tac Tyr	agc Ser	att Ile 1790	gtc Val	att Ile	aga Arg	caa Gln	5415
atc Ile 1795	tcg Ser	gac Asp	ttg Leu	atg Met	ggc Gly 1800	ctt Leu	att Ile	cct Pro	aag Lys	tat Tyr 1805	aat Asn	cac His	cta Leu	gta Val	5460
tac Tyr 1810	tct Ser	cag Gln	att Ile	cca Pro	gca Ala 1815	gct Ala	gtg Val	aaa Lys	ttg Leu	act Thr 1820	tac Tyr	caa Gln	gat Asp	gca Ala	5505
gta Val 1825	aac Asn	tta Leu	cag Gln	aac Asn	tat Tyr 1830	gta Val	gaa Glu	gaa Glu	aag Lys	ctt Leu 1835	att Ile	ccc Pro	act Thr	tgg Trp	5550
aac Asn 1840	tgg Trp	atg Met	gtc Val	agt Ser	att Ile 1845	atg Met	gat Asp	tct Ser	act Thr	gaa Glu 1850	gct Ala	caa Gln	tta Leu	cgt Arg	5595
tat Tyr 1855	ggt Gly	tct Ser	gca Ala	tta Leu	gca Ala 1860	tct Ser	gct Ala	ggt Gly	gat Asp	cct Pro 1865	gga Gly	cat His	cca Pro	aat Asn	5640
cat His 1870	cct Pro	ctt Leu	cac His	gct Ala	tct Ser 1875	cag Gln	aat Asn	tca Ser	gcg Ala	aga Arg 1880	aga Arg	gag Glu	agg Arg	atg Met	5685
act Thr 1885	gcg Ala	cga Arg	gaa Glu	gaa Glu	gct Ala 1890	agc Ser	tta Leu	cga Arg	aca Thr	ctt Leu 1895	gaa Glu	ggc Gly	aga Arg	cga Arg	5730

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cgt Arg 1900	gcc Ala	acc Thr	ttg Leu	ctt Leu	agc Ser 1905	gcc Ala	cgt Arg	caa Gln	gga Gly	atg Met 1910	atg Met	tct Ser	gca Ala	cga Arg	5775
gga Gly 1915	gac Asp	ttc Phe	cta Leu	aat Asn	tat Tyr 1920	gct Ala	ctg Leu	tct Ser	cta Leu	atg Met 1925	cgg Arg	tct Ser	cat His	aat Asn	5820
gat Asp 1930	gag Glu	cat His	tct Ser	gat Asp	gtt Val 1935	ctt Leu	cca Pro	gtt Val	ttg Leu	gat Asp 1940	gtt Val	tgc Cys	tca Ser	ttg Leu	5865
aag Lys 1945	cat His	gtg Val	gca Ala	tat Tyr	gtt Val 1950	ttt Phe	caa Gln	gca Ala	ctt Leu	ata Ile 1955	tac Tyr	tgg Trp	att Ile	aag Lys	5910
gca Ala 1960	atg Met	aat Asn	cag Gln	cag Gln	aca Thr 1965	aca Thr	ttg Leu	gat Asp	aca Thr	cct Pro 1970	caa Gln	cta Leu	gaa Glu	cgc Arg	5955
aaa Lys 1975	agg Arg	acg Thr	cga Arg	gaa Glu	ctc Leu 1980	ttg Leu	gaa Glu	ctg Leu	ggt Gly	att Ile 1985	gat Asp	aat Asn	gaa Glu	gat Asp	6000
tca Ser 1990	gaa Glu	cat His	gaa Glu	aat Asn	gat Asp 1995	gat Asp	gac Asp	acc Thr	aat Asn	caa Gln 2000	agt Ser	gct Ala	act Thr	ttg Leu	6045
aat Asn 2005	gat Asp	aag Lys	gat Asp	gat Asp	gac Asp 2010	tct Ser	ctt Leu	cct Pro	gca Ala	gaa Glu 2015	act Thr	ggc Gly	caa Gln	aac Asn	6090
cat His 2020	cca Pro	ttt Phe	ttc Phe	cga Arg	cgt Arg 2025	tca Ser	gac Asp	tcc Ser	atg Met	aca Thr 2030	ttc Phe	ctt Leu	ggg Gly	tgt Cys	6135
ata Ile 2035	ccc Pro	cca Pro	aat Asn	cca Pro	ttt Phe 2040	gaa Glu	gtg Val	cct Pro	ctg Leu	gct Ala 2045	gaa Glu	gcc Ala	atc Ile	ccc Pro	6180
ttg Leu 2050	gct Ala	gat Asp	cag Gln	cca Pro	cat His 2055	ctg Leu	ttg Leu	cag Gln	cca Pro	aat Asn 2060	gct Ala	aga Arg	aag Lys	gag Glu	6225
gat Asp 2065	ctt Leu	ttt Phe	ggc Gly	cgt Arg	cca Pro 2070	agt Ser	cag Gln	ggt Gly	ctt Leu	tat Tyr 2075	tct Ser	tca Ser	tct Ser	gcc Ala	6270
agt Ser 2080	agt Ser	ggg Gly	aaa Lys	tgt Cys	tta Leu 2085	atg Met	gag Glu	gtt Val	aca Thr	gtg Val 2090	gat Asp	aga Arg	aac Asn	tgc Cys	6315
cta Leu 2095	gag Glu	gtt Val	ctt Leu	cca Pro	aca Thr 2100	aaa Lys	atg Met	tct Ser	tat Tyr	gct Ala 2105	gcc Ala	aat Asn	ctg Leu	aaa Lys	6360
aat Asn 2110	gta Val	atg Met	aac Asn	atg Met	caa Gln 2115	aac Asn	cgg Arg	caa Gln	aaa Lys	aaa Lys 2120	gaa Glu	ggg Gly	gaa Glu	gaa Glu	6405
cag Gln 2125	ccc Pro	gtg Val	ctg Leu	cca Pro	gaa Glu 2130	gaa Glu	act Thr	gag Glu	agt Ser	tca Ser 2135	aaa Lys	cca Pro	ggg Gly	cca Pro	6450
tct Ser 2140	gct Ala	cat His	gat Asp	ctt Leu	gct Ala 2145	gca Ala	caa Gln	tta Leu	aaa Lys	agt Ser 2150	agc Ser	tta Leu	cta Leu	gca Ala	6495



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gaa Glu 2155	ata Ile	gga Gly	ctt Leu	act Thr	gaa Glu 2160	agt Ser	gaa Glu	ggg Gly	cca Pro	cct Pro 2165	ctc Leu	aca Thr	tct Ser	ttc Phe	6540
agg Arg 2170	cca Pro	cag Gln	tgt Cys	agc Ser	ttt Phe 2175	atg Met	gga Gly	atg Met	gtt Val	att Ile 2180	tcc Ser	cat His	gat Asp	atg Met	6585
ctg Leu 2185	cta Leu	gga Gly	cgt Arg	tgg Trp	cgc Arg 2190	ctt Leu	tct Ser	tta Leu	gaa Glu	ctg Leu 2195	ttc Phe	ggc Gly	agg Arg	gta Val	6630
ttc Phe 2200	atg Met	gaa Glu	gat Asp	gtt Val	gga Gly 2205	gca Ala	gaa Glu	cct Pro	gga Gly	tca Ser 2210	atc Ile	cta Leu	act Thr	gaa Glu	6675
ttg Leu 2215	ggt Gly	ggt Gly	ttt Phe	gag Glu	gta Val 2220	aaa Lys	gaa Glu	tca Ser	aaa Lys	ttc Phe 2225	cgc Arg	aga Arg	gaa Glu	atg Met	6720
gaa Glu 2230	aaa Lys	ctg Leu	aga Arg	aac Asn	cag Gln 2235	cag Gln	tca Ser	aga Arg	gat Asp	ttg Leu 2240	tca Ser	cta Leu	gag Glu	gtt Val	6765
gat Asp 2245	cgg Arg	gat Asp	cga Arg	gat Asp	ctt Leu 2250	ctc Leu	att Ile	cag Gln	cag Gln	act Thr 2255	atg Met	agg Arg	cag Gln	ctt Leu	6810
aac Asn 2260	aat Asn	cac His	ttt Phe	ggt Gly	cga Arg 2265	aga Arg	tgt Cys	gct Ala	act Thr	aca Thr 2270	cca Pro	atg Met	gct Ala	gta Val	6855
cac His 2275	aga Arg	gta Val	aaa Lys	gtc Val	aca Thr 2280	ttt Phe	aag Lys	gat Asp	gag Glu	cca Pro 2285	gga Gly	gag Glu	ggc Gly	agt Ser	6900
ggt Gly 2290	gta Val	gca Ala	cga Arg	agt Ser	ttt Phe 2295	tat Tyr	aca Thr	gcc Ala	att Ile	gca Ala 2300	caa Gln	gca Ala	ttt Phe	tta Leu	6945
tca Ser 2305	aat Asn	gaa Glu	aaa Lys	ttg Leu	cca Pro 2310	aat Asn	cta Leu	gag Glu	tgt Cys	atc Ile 2315	caa Gln	aat Asn	gcc Ala	aac Asn	6990
aaa Lys 2320	ggc Gly	acc Thr	cac His	aca Thr	agt Ser 2325	tta Leu	atg Met	cag Gln	aga Arg	tta Leu 2330	agg Arg	aac Asn	cga Arg	gga Gly	7035
gag Glu 2335	aga Arg	gac Asp	cgg Arg	gaa Glu	agg Arg 2340	gag Glu	aga Arg	gaa Glu	agg Arg	gaa Glu 2345	atg Met	agg Arg	agg Arg	agt Ser	7080
agt Ser 2350	ggt Gly	ttg Leu	cga Arg	gca Ala	ggt Gly 2355	tct Ser	cgg Arg	agg Arg	gac Asp	cgg Arg 2360	gat Asp	aga Arg	gac Asp	ttt Phe	7125
aga Arg 2365	aga Arg	cag Gln	ctt Leu	tcc Ser	atc Ile 2370	gac Asp	act Thr	agg Arg	ccc Pro	ttt Phe 2375	aga Arg	cca Pro	gcc Ala	tct Ser	7170
gaa Glu 2380	ggg Gly	aat Asn	cct Pro	agc Ser	gat Asp 2385	gat Asp	cct Pro	gag Glu	cct Pro	ttg Leu 2390	cca Pro	gca Ala	cat His	cgg Arg	7215
cag Gln 2395	gca Ala	ctt Leu	gga Gly	gag Glu	agg Arg 2400	ctt Leu	tat Tyr	cct Pro	cgt Arg	gta Val 2405	caa Gln	gca Ala	atg Met	caa Gln	7260

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cca Pro 2410	gca Ala	ttt Phe	gca Ala	agt Ser	aaa Lys 2415	atc Ile	act Thr	ggc Gly	atg Met	ttg Leu 2420	ttg Leu	gaa Glu	tta Leu	tcc Ser	7305
cca Pro 2425	gct Ala	cag Gln	ctg Leu	ctt Leu	ctc Leu 2430	ctt Leu	cta Leu	gca Ala	agt Ser	gag Glu 2435	gat Asp	tct Ser	ctg Leu	aga Arg	7350
gca Ala 2440	aga Arg	gtg Val	gat Asp	gag Glu	gcc Ala 2445	atg Met	gaa Glu	ctc Leu	att Ile	att Ile 2450	gca Ala	cat His	gga Gly	cgg Arg	7395
gaa Glu 2455	aat Asn	gga Gly	gct Ala	gat Asp	agt Ser 2460	atc Ile	ctg Leu	gat Asp	ctt Leu	gga Gly 2465	tta Leu	gta Val	gac Asp	tcc Ser	7440
tca Ser 2470	gaa Glu	aag Lys	gta Val	cag Gln	cag Gln 2475	gaa Glu	aac Asn	cga Arg	aag Lys	cgc Arg 2480	cat His	ggc Gly	tct Ser	agt Ser	7485
cga Arg 2485	agt Ser	gta Val	gta Val	gat Asp	atg Met 2490	gat Asp	tta Leu	gat Asp	gat Asp	aca Thr 2495	gat Asp	gat Asp	ggt Gly	gat Asp	7530
gac Asp 2500	aat Asn	gcc Ala	cct Pro	ttg Leu	ttt Phe 2505	tac Tyr	caa Gln	cct Pro	ggg Gly	aaa Lys 2510	aga Arg	gga Gly	ttt Phe	tat Tyr	7575
act Thr 2515	cca Pro	agg Arg	cct Pro	ggc Gly	aag Lys 2520	aac Asn	aca Thr	gaa Glu	gca Ala	agg Arg 2525	ttg Leu	aat Asn	tgt Cys	ttc Phe	7620
aga Arg 2530	aac Asn	att Ile	ggc Gly	agg Arg	att Ile 2535	ctt Leu	gga Gly	cta Leu	tgt Cys	ctg Leu 2540	tta Leu	cag Gln	aat Asn	gaa Glu	7665
ctc Leu 2545	tgt Cys	cct Pro	atc Ile	aca Thr	ttg Leu 2550	aat Asn	aga Arg	cat His	gta Val	att Ile 2555	aaa Lys	gta Val	ttg Leu	ctt Leu	7710
ggt Gly 2560	aga Arg	aaa Lys	gtc Val	aat Asn	tgg Trp 2565	cat His	gat Asp	ttt Phe	gct Ala	ttt Phe 2570	ttt Phe	gat Asp	cct Pro	gta Val	7755
atg Met 2575	tat Tyr	gag Glu	agt Ser	ttg Leu	cgg Arg 2580	caa Gln	cta Leu	atc Ile	ctc Leu	gcg Ala 2585	tct Ser	cag Gln	agt Ser	tca Ser	7800
gat Asp 2590	gct Ala	gat Asp	gct Ala	gtt Val	ttc Phe 2595	tca Ser	gca Ala	atg Met	gat Asp	ttg Leu 2600	gca Ala	ttt Phe	gca Ala	att Ile	7845
gac Asp 2605	ctg Leu	tgt Cys	aaa Lys	gaa Glu	gaa Glu 2610	ggt Gly	gga Gly	gga Gly	cag Gln	gtt Val 2615	gaa Glu	ctc Leu	att Ile	cct Pro	7890
aat Asn 2620	ggt Gly	gta Val	aat Asn	ata Ile	cca Pro 2625	gtc Val	act Thr	cca Pro	cag Gln	aat Asn 2630	gta Val	tat Tyr	gag Glu	tat Tyr	7935
gtg Val 2635	cgg Arg	aaa Lys	tac Tyr	gca Ala	gaa Glu 2640	cac His	aga Arg	atg Met	ttg Leu	gta Val 2645	gtt Val	gca Ala	gaa Glu	cag Gln	7980
ccc Pro 2650	tta Leu	cat His	gca Ala	atg Met	agg Arg 2655	aaa Lys	ggt Gly	cta Leu	cta Leu	gat Asp 2660	gtg Val	ctt Leu	cca Pro	aaa Lys	8025

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aat Asn 2665	tca Ser	tta Leu	gaa Glu	gat Asp	tta Leu 2670	acg Thr	gca Ala	gaa Glu	gat Asp	ttt Phe 2675	agg Arg	ctt Leu	ttg Leu	gta Val	8070
aat Asn 2680	ggc Gly	tgc Cys	ggt Gly	gaa Glu	gtc Val 2685	aat Asn	gtg Val	caa Gln	atg Met	ctg Leu 2690	atc Ile	agt Ser	ttt Phe	acc Thr	8115
tct Ser 2695	ttc Phe	aat Asn	gat Asp	gaa Glu	tca Ser 2700	gga Gly	gaa Glu	aat Asn	gct Ala	gag Glu 2705	aag Lys	ctt Leu	ctg Leu	cag Gln	8160
ttc Phe 2710	aag Lys	cgt Arg	tgg Trp	ttc Phe	tgg Trp 2715	tca Ser	ata Ile	gta Val	gag Glu	aag Lys 2720	atg Met	agc Ser	atg Met	aca Thr	8205
gaa Glu 2725	cga Arg	caa Gln	gat Asp	ctt Leu	gtt Val 2730	tac Tyr	ttt Phe	tgg Trp	aca Thr	tca Ser 2735	agc Ser	cca Pro	tca Ser	ctg Leu	8250
cca Pro 2740	gcc Ala	agt Ser	gaa Glu	gaa Glu	gga Gly 2745	ttc Phe	cag Gln	cct Pro	atg Met	ccc Pro 2750	tca Ser	atc Ile	aca Thr	ata Ile	8295
aga Arg 2755	cca Pro	cca Pro	gat Asp	gac Asp	caa Gln 2760	cat His	ctt Leu	cct Pro	act Thr	gca Ala 2765	aat Asn	act Thr	tgc Cys	att Ile	8340
tct Ser 2770	cga Arg	ctt Leu	tac Tyr	gtc Val	cca Pro 2775	ctc Leu	tat Tyr	tcc Ser	tct Ser	aaa Lys 2780	cag Gln	att Ile	ctc Leu	aaa Lys	8385
cag Gln 2785	aaa Lys	ttg Leu	tta Leu	ctc Leu	gcc Ala 2790	att Ile	aag Lys	acc Thr	aag Lys	aat Asn 2795	ttt Phe	ggt Gly	ttt Phe	gtg Val	8430
tagagtataa aaagtgtgta ttgctgtgta atattactag caaattttgt agattttttt 8490															
ccatttgtct ataaaagtta aagtttatgg aagttaatgc tgtcataccc ccctgggtgg 8550															
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gcactagcaa catttggtgta tattgggttg ctagtcacca acttctgggt ctaacccag 8670															
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<210> 64  
 <211> 2799  
 <212> PRT  
 <213> homo sapiens

<400> 64

Met Thr Ser Ile His Phe Val Val His Pro Leu Pro Gly Thr Glu Asp  
 1 5 10 15

Gln Leu Asn Asp Arg Leu Arg Glu Val Ser Glu Lys Leu Asn Lys Tyr  
 20 25 30

Asn Leu Asn Ser His Pro Pro Leu Asn Val Leu Glu Gln Ala Thr Ile

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35

40

45

Lys Gln Cys Val Val Gly Pro Asn His Ala Ala Phe Leu Leu Glu Asp  
50 55 60

Gly Arg Val Cys Arg Ile Gly Phe Ser Val Gln Pro Asp Arg Leu Glu  
65 70 75 80

Leu Gly Lys Pro Asp Asn Asn Asp Gly Ser Lys Leu Asn Ser Asn Ser  
85 90 95

Gly Ala Gly Arg Thr Ser Arg Pro Gly Arg Thr Ser Asp Ser Pro Trp  
100 105 110

Phe Leu Ser Gly Ser Glu Thr Leu Gly Arg Leu Ala Gly Asn Thr Leu  
115 120 125

Gly Ser Arg Trp Ser Ser Gly Val Gly Gly Ser Gly Gly Gly Ser Ser  
130 135 140

Gly Arg Ser Ser Ala Gly Ala Arg Asp Ser Arg Arg Gln Thr Arg Val  
145 150 155 160

Ile Arg Thr Gly Arg Asp Arg Gly Ser Gly Leu Leu Gly Ser Gln Pro  
165 170 175

Gln Pro Val Ile Pro Ala Ser Val Ile Pro Glu Glu Leu Ile Ser Gln  
180 185 190

Ala Gln Val Val Leu Gln Gly Lys Ser Arg Ser Val Ile Ile Arg Glu  
195 200 205

Leu Gln Arg Thr Asn Leu Asp Val Asn Leu Ala Val Asn Asn Leu Leu  
210 215 220

Ser Arg Asp Asp Glu Asp Gly Asp Asp Gly Asp Asp Thr Ala Ser Glu  
225 230 235 240

Ser Tyr Leu Pro Gly Glu Asp Leu Met Ser Leu Leu Asp Ala Asp Ile  
245 250 255

His Ser Ala His Pro Ser Val Ile Ile Asp Ala Asp Ala Met Phe Ser  
260 265 270

Glu Asp Ile Ser Tyr Phe Gly Tyr Pro Ser Phe Arg Arg Ser Ser Leu  
275 280 285

Ser Arg Leu Gly Ser Ser Arg Val Leu Leu Leu Pro Leu Glu Arg Asp  
290 295 300

Ser Glu Leu Leu Arg Glu Arg Glu Ser Val Leu Arg Leu Arg Glu Arg  
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122257 sequence listing May 10 2006.ST25.txt  
 305 310 315 320

Arg Trp Leu Asp Gly Ala Ser Phe Asp Asn Glu Arg Gly Ser Thr Ser  
 325 330 335

Lys Glu Gly Glu Pro Asn Leu Asp Lys Lys Asn Thr Pro Val Gln Ser  
 340 345 350

Pro Val Ser Leu Gly Glu Asp Leu Gln Trp Trp Pro Asp Lys Asp Gly  
 355 360 365

Thr Lys Phe Ile Cys Ile Gly Ala Leu Tyr Ser Glu Leu Leu Ala Val  
 370 375 380

Ser Ser Lys Gly Glu Leu Tyr Gln Trp Lys Trp Ser Glu Ser Glu Pro  
 385 390 395 400

Tyr Arg Asn Ala Gln Asn Pro Ser Leu His His Pro Arg Ala Thr Phe  
 405 410 415

Leu Gly Leu Thr Asn Glu Lys Ile Val Leu Leu Ser Ala Asn Ser Ile  
 420 425 430

Arg Ala Thr Val Ala Thr Glu Asn Asn Lys Val Ala Thr Trp Val Asp  
 435 440 445

Glu Thr Leu Ser Ser Val Ala Ser Lys Leu Glu His Thr Ala Gln Thr  
 450 455 460

Tyr Ser Glu Leu Gln Gly Glu Arg Ile Val Ser Leu His Cys Cys Ala  
 465 470 475 480

Leu Tyr Thr Cys Ala Gln Leu Glu Asn Ser Leu Tyr Trp Trp Gly Val  
 485 490 495

Val Pro Phe Ser Gln Arg Lys Lys Met Leu Glu Lys Ala Arg Ala Lys  
 500 505 510

Asn Lys Lys Pro Lys Ser Ser Ala Gly Ile Ser Ser Met Pro Asn Ile  
 515 520 525

Thr Val Gly Thr Gln Val Cys Leu Arg Asn Asn Pro Leu Tyr His Ala  
 530 535 540

Gly Ala Val Ala Phe Ser Ile Ser Ala Gly Ile Pro Lys Val Gly Val  
 545 550 555 560

Leu Met Glu Ser Val Trp Asn Met Asn Asp Ser Cys Arg Phe Gln Leu  
 565 570 575

Arg Ser Pro Glu Ser Leu Lys Asn Met Glu Lys Ala Ser Lys Thr Thr  
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Glu Ala Lys Pro Glu Ser Lys Gln Glu Pro Val Lys Thr Glu Met Gly  
595 600 605

Pro Pro Pro Ser Pro Ala Ser Thr Cys Ser Asp Ala Ser Ser Ile Ala  
610 615 620

Ser Ser Ala Ser Met Pro Tyr Lys Arg Arg Arg Ser Thr Pro Ala Pro  
625 630 635 640

Lys Glu Glu Glu Lys Val Asn Glu Glu Gln Trp Ser Leu Arg Glu Val  
645 650 655

Val Phe Val Glu Asp Val Lys Asn Val Pro Val Gly Lys Val Leu Lys  
660 665 670

Val Asp Gly Ala Tyr Val Ala Val Lys Phe Pro Gly Thr Ser Ser Asn  
675 680 685

Thr Asn Cys Gln Asn Ser Ser Gly Pro Asp Ala Asp Pro Ser Ser Leu  
690 695 700

Leu Gln Asp Cys Arg Leu Leu Arg Ile Asp Glu Leu Gln Val Val Lys  
705 710 715 720

Thr Gly Gly Thr Pro Lys Val Pro Asp Cys Phe Gln Arg Thr Pro Lys  
725 730 735

Lys Leu Cys Ile Pro Glu Lys Thr Glu Ile Leu Ala Val Asn Val Asp  
740 745 750

Ser Lys Gly Val His Ala Val Leu Lys Thr Gly Asn Trp Val Arg Tyr  
755 760 765

Cys Ile Phe Asp Leu Ala Thr Gly Lys Ala Glu Gln Glu Asn Asn Phe  
770 775 780

Pro Thr Ser Ser Ile Ala Phe Leu Gly Gln Asn Glu Arg Asn Val Ala  
785 790 795 800

Ile Phe Thr Ala Gly Gln Glu Ser Pro Ile Ile Leu Arg Asp Gly Asn  
805 810 815

Gly Thr Ile Tyr Pro Met Ala Lys Asp Cys Met Gly Gly Ile Arg Asp  
820 825 830

Pro Asp Trp Leu Asp Leu Pro Pro Ile Ser Ser Leu Gly Met Gly Val  
835 840 845

His Ser Leu Ile Asn Leu Pro Ala Asn Ser Thr Ile Lys Lys Lys Ala

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850

855

860

Ala Val Ile Ile Met Ala Val Glu Lys Gln Thr Leu Met Gln His Ile  
865 870 875 880

Leu Arg Cys Asp Tyr Glu Ala Cys Arg Gln Tyr Leu Met Asn Leu Glu  
885 890 895

Gln Ala Val Val Leu Glu Gln Asn Leu Gln Met Leu Gln Thr Phe Ile  
900 905 910

Ser His Arg Cys Asp Gly Asn Arg Asn Ile Leu His Ala Cys Val Ser  
915 920 925

Val Cys Phe Pro Thr Ser Asn Lys Glu Thr Lys Glu Glu Glu Glu Ala  
930 935 940

Glu Arg Ser Glu Arg Asn Thr Phe Ala Glu Arg Leu Ser Ala Val Glu  
945 950 955 960

Ala Ile Ala Asn Ala Ile Ser Val Val Ser Ser Asn Gly Pro Gly Asn  
965 970 975

Arg Ala Gly Ser Ser Ser Ser Arg Ser Leu Arg Leu Arg Glu Met Met  
980 985 990

Arg Arg Ser Leu Arg Ala Ala Gly Leu Gly Arg His Glu Ala Gly Ala  
995 1000 1005

Ser Ser Ser Asp His Gln Asp Pro Val Ser Pro Pro Ile Ala Pro  
1010 1015 1020

Pro Ser Trp Val Pro Asp Pro Pro Ala Met Asp Pro Asp Gly Asp  
1025 1030 1035

Ile Asp Phe Ile Leu Ala Pro Ala Val Gly Ser Leu Thr Thr Ala  
1040 1045 1050

Ala Thr Gly Thr Gly Gln Gly Pro Ser Thr Ser Thr Ile Pro Gly  
1055 1060 1065

Pro Ser Thr Glu Pro Ser Val Val Glu Ser Lys Asp Arg Lys Ala  
1070 1075 1080

Asn Ala His Phe Ile Leu Lys Leu Leu Cys Asp Ser Val Val Leu  
1085 1090 1095

Gln Pro Tyr Leu Arg Glu Leu Leu Ser Ala Lys Asp Ala Arg Gly  
1100 1105 1110

Met Thr Pro Phe Met Ser Ala Val Ser Gly Arg Ala Tyr Pro Ala  
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1115 122257 sequence listing May 10 2006.ST25.txt 1125 1125

Ala	Ile	Thr	Ile	Leu	Glu	Thr	Ala	Gln	Lys	Ile	Ala	Lys	Ala	Glu
1130						1135					1140			
Ile	Ser	Ser	Ser	Glu	Lys	Glu	Glu	Asp	Val	Phe	Met	Gly	Met	Val
1145						1150					1155			
Cys	Pro	Ser	Gly	Thr	Asn	Pro	Asp	Asp	Ser	Pro	Leu	Tyr	Val	Leu
1160						1165					1170			
Cys	Cys	Asn	Asp	Thr	Cys	Ser	Phe	Thr	Trp	Thr	Gly	Ala	Glu	His
1175						1180					1185			
Ile	Asn	Gln	Asp	Ile	Phe	Glu	Cys	Arg	Thr	Cys	Gly	Leu	Leu	Glu
1190						1195					1200			
Ser	Leu	Cys	Cys	Cys	Thr	Glu	Cys	Ala	Arg	Val	Cys	His	Lys	Gly
1205						1210					1215			
His	Asp	Cys	Lys	Leu	Lys	Arg	Thr	Ser	Pro	Thr	Ala	Tyr	Cys	Asp
1220						1225					1230			
Cys	Trp	Glu	Lys	Cys	Lys	Cys	Lys	Thr	Leu	Ile	Ala	Gly	Gln	Lys
1235						1240					1245			
Ser	Ala	Arg	Leu	Asp	Leu	Leu	Tyr	Arg	Leu	Leu	Thr	Ala	Thr	Asn
1250						1255					1260			
Leu	Val	Thr	Leu	Pro	Asn	Ser	Arg	Gly	Glu	His	Leu	Leu	Leu	Phe
1265						1270					1275			
Leu	Val	Gln	Thr	Val	Ala	Arg	Gln	Thr	Val	Glu	His	Cys	Gln	Tyr
1280						1285					1290			
Arg	Pro	Pro	Arg	Ile	Arg	Glu	Asp	Arg	Asn	Arg	Lys	Thr	Ala	Ser
1295						1300					1305			
Pro	Glu	Asp	Ser	Asp	Met	Pro	Asp	His	Asp	Leu	Glu	Pro	Pro	Arg
1310						1315					1320			
Phe	Ala	Gln	Leu	Ala	Leu	Glu	Arg	Val	Leu	Gln	Asp	Trp	Asn	Ala
1325						1330					1335			
Leu	Lys	Ser	Met	Ile	Met	Phe	Gly	Ser	Gln	Glu	Asn	Lys	Asp	Pro
1340						1345					1350			
Leu	Ser	Ala	Ser	Ser	Arg	Ile	Gly	His	Leu	Leu	Pro	Glu	Glu	Gln
1355						1360					1365			
Val	Tyr	Leu	Asn	Gln	Gln	Ser	Gly	Thr	Ile	Arg	Leu	Asp	Cys	Phe



1370 122257 sequence listing May 10 2006.ST25.txt 1380  
1375

Thr His Cys Leu Ile Val Lys Cys Thr Ala Asp Ile Leu Leu Leu  
1385 1390 1395

Asp Thr Leu Leu Gly Thr Leu Val Lys Glu Leu Gln Asn Lys Tyr  
1400 1405 1410

Thr Pro Gly Arg Arg Glu Glu Ala Ile Ala Val Thr Met Arg Phe  
1415 1420 1425

Leu Arg Ser Val Ala Arg Val Phe Val Ile Leu Ser Val Glu Met  
1430 1435 1440

Ala Ser Ser Lys Lys Lys Asn Asn Phe Ile Pro Gln Pro Ile Gly  
1445 1450 1455

Lys Cys Lys Arg Val Phe Gln Ala Leu Leu Pro Tyr Ala Val Glu  
1460 1465 1470

Glu Leu Cys Asn Val Ala Glu Ser Leu Ile Val Pro Val Arg Met  
1475 1480 1485

Gly Ile Ala Arg Pro Thr Ala Pro Phe Thr Leu Ala Ser Thr Ser  
1490 1495 1500

Ile Asp Ala Met Gln Gly Ser Glu Glu Leu Phe Ser Val Glu Pro  
1505 1510 1515

Leu Pro Pro Arg Pro Ser Ser Asp Gln Ser Ser Ser Ser Ser Gln  
1520 1525 1530

Ser Gln Ser Ser Tyr Ile Ile Arg Asn Pro Gln Gln Arg Arg Ile  
1535 1540 1545

Ser Gln Ser Gln Pro Val Arg Gly Arg Asp Glu Glu Gln Asp Asp  
1550 1555 1560

Ile Val Ser Ala Asp Val Glu Glu Val Glu Val Val Glu Gly Val  
1565 1570 1575

Ala Gly Glu Glu Asp His His Asp Glu Gln Glu Glu His Gly Glu  
1580 1585 1590

Glu Asn Ala Glu Ala Glu Gly Gln His Asp Glu His Asp Glu Asp  
1595 1600 1605

Gly Ser Asp Met Glu Leu Asp Leu Leu Ala Ala Ala Glu Thr Glu  
1610 1615 1620

Ser Asp Ser Glu Ser Asn His Ser Asn Gln Asp Asn Ala Ser Gly  
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122257 sequence listing May 10 2006.ST25.txt  
1625 1630 1635

Arg	Arg	Ser	Val	Val	Thr	Ala	Ala	Thr	Ala	Gly	Ser	Glu	Ala	Gly
1640						1645					1650			
Ala	Ser	Ser	Val	Pro	Ala	Phe	Phe	Ser	Glu	Asp	Asp	Ser	Gln	Ser
1655						1660					1665			
Asn	Asp	Ser	Ser	Asp	Ser	Asp	Ser	Ser	Ser	Ser	Gln	Ser	Asp	Asp
1670						1675					1680			
Ile	Glu	Gln	Glu	Thr	Phe	Met	Leu	Asp	Glu	Pro	Leu	Glu	Arg	Thr
1685						1690					1695			
Thr	Asn	Ser	Ser	His	Ala	Asn	Gly	Ala	Ala	Gln	Ala	Pro	Arg	Ser
1700						1705					1710			
Met	Gln	Trp	Ala	Val	Arg	Asn	Thr	Gln	His	Gln	Arg	Ala	Ala	Ser
1715						1720					1725			
Thr	Ala	Pro	Ser	Ser	Thr	Ser	Thr	Pro	Ala	Ala	Ser	Ser	Ala	Gly
1730						1735					1740			
Leu	Ile	Tyr	Ile	Asp	Pro	Ser	Asn	Leu	Arg	Arg	Ser	Gly	Thr	Ile
1745						1750					1755			
Ser	Thr	Ser	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Leu	Glu	Ala	Ser	Asn
1760						1765					1770			
Ala	Ser	Ser	Tyr	Leu	Thr	Ser	Ala	Ser	Ser	Leu	Ala	Arg	Ala	Tyr
1775						1780					1785			
Ser	Ile	Val	Ile	Arg	Gln	Ile	Ser	Asp	Leu	Met	Gly	Leu	Ile	Pro
1790						1795					1800			
Lys	Tyr	Asn	His	Leu	Val	Tyr	Ser	Gln	Ile	Pro	Ala	Ala	Val	Lys
1805						1810					1815			
Leu	Thr	Tyr	Gln	Asp	Ala	Val	Asn	Leu	Gln	Asn	Tyr	Val	Glu	Glu
1820						1825					1830			
Lys	Leu	Ile	Pro	Thr	Trp	Asn	Trp	Met	Val	Ser	Ile	Met	Asp	Ser
1835						1840					1845			
Thr	Glu	Ala	Gln	Leu	Arg	Tyr	Gly	Ser	Ala	Leu	Ala	Ser	Ala	Gly
1850						1855					1860			
Asp	Pro	Gly	His	Pro	Asn	His	Pro	Leu	His	Ala	Ser	Gln	Asn	Ser
1865						1870					1875			
Ala	Arg	Arg	Glu	Arg	Met	Thr	Ala	Arg	Glu	Glu	Ala	Ser	Leu	Arg

1880 122257 sequence listing May 10 2006.ST25.txt  
1885 1890

Thr	Leu	Glu	Gly	Arg	Arg	Arg	Ala	Thr	Leu	Leu	Ser	Ala	Arg	Gln
1895						1900					1905			
Gly	Met	Met	Ser	Ala	Arg	Gly	Asp	Phe	Leu	Asn	Tyr	Ala	Leu	Ser
1910						1915					1920			
Leu	Met	Arg	Ser	His	Asn	Asp	Glu	His	Ser	Asp	Val	Leu	Pro	Val
1925						1930					1935			
Leu	Asp	Val	Cys	Ser	Leu	Lys	His	Val	Ala	Tyr	Val	Phe	Gln	Ala
1940						1945					1950			
Leu	Ile	Tyr	Trp	Ile	Lys	Ala	Met	Asn	Gln	Gln	Thr	Thr	Leu	Asp
1955						1960					1965			
Thr	Pro	Gln	Leu	Glu	Arg	Lys	Arg	Thr	Arg	Glu	Leu	Leu	Glu	Leu
1970						1975					1980			
Gly	Ile	Asp	Asn	Glu	Asp	Ser	Glu	His	Glu	Asn	Asp	Asp	Asp	Thr
1985						1990					1995			
Asn	Gln	Ser	Ala	Thr	Leu	Asn	Asp	Lys	Asp	Asp	Asp	Ser	Leu	Pro
2000						2005					2010			
Ala	Glu	Thr	Gly	Gln	Asn	His	Pro	Phe	Phe	Arg	Arg	Ser	Asp	Ser
2015						2020					2025			
Met	Thr	Phe	Leu	Gly	Cys	Ile	Pro	Pro	Asn	Pro	Phe	Glu	Val	Pro
2030						2035					2040			
Leu	Ala	Glu	Ala	Ile	Pro	Leu	Ala	Asp	Gln	Pro	His	Leu	Leu	Gln
2045						2050					2055			
Pro	Asn	Ala	Arg	Lys	Glu	Asp	Leu	Phe	Gly	Arg	Pro	Ser	Gln	Gly
2060						2065					2070			
Leu	Tyr	Ser	Ser	Ser	Ala	Ser	Ser	Gly	Lys	Cys	Leu	Met	Glu	Val
2075						2080					2085			
Thr	Val	Asp	Arg	Asn	Cys	Leu	Glu	Val	Leu	Pro	Thr	Lys	Met	Ser
2090						2095					2100			
Tyr	Ala	Ala	Asn	Leu	Lys	Asn	Val	Met	Asn	Met	Gln	Asn	Arg	Gln
2105						2110					2115			
Lys	Lys	Glu	Gly	Glu	Glu	Gln	Pro	Val	Leu	Pro	Glu	Glu	Thr	Glu
2120						2125					2130			
Ser	Ser	Lys	Pro	Gly	Pro	Ser	Ala	His	Asp	Leu	Ala	Ala	Gln	Leu

2135 122257 sequence listing May 10 2006.ST25.txt  
2140 2145

Lys	Ser	Ser	Leu	Leu	Ala	Glu	Ile	Gly	Leu	Thr	Glu	Ser	Glu	Gly
2150						2155					2160			
Pro	Pro	Leu	Thr	Ser	Phe	Arg	Pro	Gln	Cys	Ser	Phe	Met	Gly	Met
2165						2170					2175			
Val	Ile	Ser	His	Asp	Met	Leu	Leu	Gly	Arg	Trp	Arg	Leu	Ser	Leu
2180						2185					2190			
Glu	Leu	Phe	Gly	Arg	Val	Phe	Met	Glu	Asp	Val	Gly	Ala	Glu	Pro
2195						2200					2205			
Gly	Ser	Ile	Leu	Thr	Glu	Leu	Gly	Gly	Phe	Glu	Val	Lys	Glu	Ser
2210						2215					2220			
Lys	Phe	Arg	Arg	Glu	Met	Glu	Lys	Leu	Arg	Asn	Gln	Gln	Ser	Arg
2225						2230					2235			
Asp	Leu	Ser	Leu	Glu	Val	Asp	Arg	Asp	Arg	Asp	Leu	Leu	Ile	Gln
2240						2245					2250			
Gln	Thr	Met	Arg	Gln	Leu	Asn	Asn	His	Phe	Gly	Arg	Arg	Cys	Ala
2255						2260					2265			
Thr	Thr	Pro	Met	Ala	Val	His	Arg	Val	Lys	Val	Thr	Phe	Lys	Asp
2270						2275					2280			
Glu	Pro	Gly	Glu	Gly	Ser	Gly	Val	Ala	Arg	Ser	Phe	Tyr	Thr	Ala
2285						2290					2295			
Ile	Ala	Gln	Ala	Phe	Leu	Ser	Asn	Glu	Lys	Leu	Pro	Asn	Leu	Glu
2300						2305					2310			
Cys	Ile	Gln	Asn	Ala	Asn	Lys	Gly	Thr	His	Thr	Ser	Leu	Met	Gln
2315						2320					2325			
Arg	Leu	Arg	Asn	Arg	Gly	Glu	Arg	Asp	Arg	Glu	Arg	Glu	Arg	Glu
2330						2335					2340			
Arg	Glu	Met	Arg	Arg	Ser	Ser	Gly	Leu	Arg	Ala	Gly	Ser	Arg	Arg
2345						2350					2355			
Asp	Arg	Asp	Arg	Asp	Phe	Arg	Arg	Gln	Leu	Ser	Ile	Asp	Thr	Arg
2360						2365					2370			
Pro	Phe	Arg	Pro	Ala	Ser	Glu	Gly	Asn	Pro	Ser	Asp	Asp	Pro	Glu
2375						2380					2385			
Pro	Leu	Pro	Ala	His	Arg	Gln	Ala	Leu	Gly	Glu	Arg	Leu	Tyr	Pro

2390 122257 sequence listing May 10 2006.ST25.txt  
2395 2400

Arg	Val	Gln	Ala	Met	Gln	Pro	Ala	Phe	Ala	Ser	Lys	Ile	Thr	Gly
2405						2410					2415			
Met	Leu	Leu	Glu	Leu	Ser	Pro	Ala	Gln	Leu	Leu	Leu	Leu	Leu	Ala
2420						2425					2430			
Ser	Glu	Asp	Ser	Leu	Arg	Ala	Arg	Val	Asp	Glu	Ala	Met	Glu	Leu
2435						2440					2445			
Ile	Ile	Ala	His	Gly	Arg	Glu	Asn	Gly	Ala	Asp	Ser	Ile	Leu	Asp
2450						2455					2460			
Leu	Gly	Leu	Val	Asp	Ser	Ser	Glu	Lys	Val	Gln	Gln	Glu	Asn	Arg
2465						2470					2475			
Lys	Arg	His	Gly	Ser	Ser	Arg	Ser	Val	Val	Asp	Met	Asp	Leu	Asp
2480						2485					2490			
Asp	Thr	Asp	Asp	Gly	Asp	Asp	Asn	Ala	Pro	Leu	Phe	Tyr	Gln	Pro
2495						2500					2505			
Gly	Lys	Arg	Gly	Phe	Tyr	Thr	Pro	Arg	Pro	Gly	Lys	Asn	Thr	Glu
2510						2515					2520			
Ala	Arg	Leu	Asn	Cys	Phe	Arg	Asn	Ile	Gly	Arg	Ile	Leu	Gly	Leu
2525						2530					2535			
Cys	Leu	Leu	Gln	Asn	Glu	Leu	Cys	Pro	Ile	Thr	Leu	Asn	Arg	His
2540						2545					2550			
Val	Ile	Lys	Val	Leu	Leu	Gly	Arg	Lys	Val	Asn	Trp	His	Asp	Phe
2555						2560					2565			
Ala	Phe	Phe	Asp	Pro	Val	Met	Tyr	Glu	Ser	Leu	Arg	Gln	Leu	Ile
2570						2575					2580			
Leu	Ala	Ser	Gln	Ser	Ser	Asp	Ala	Asp	Ala	Val	Phe	Ser	Ala	Met
2585						2590					2595			
Asp	Leu	Ala	Phe	Ala	Ile	Asp	Leu	Cys	Lys	Glu	Glu	Gly	Gly	Gly
2600						2605					2610			
Gln	Val	Glu	Leu	Ile	Pro	Asn	Gly	Val	Asn	Ile	Pro	Val	Thr	Pro
2615						2620					2625			
Gln	Asn	Val	Tyr	Glu	Tyr	Val	Arg	Lys	Tyr	Ala	Glu	His	Arg	Met
2630						2635					2640			
Leu	Val	Val	Ala	Glu	Gln	Pro	Leu	His	Ala	Met	Arg	Lys	Gly	Leu

122257 sequence listing May 10 2006.ST25.txt  
 2645 2650 2655

Leu Asp Val Leu Pro Lys Asn Ser Leu Glu Asp Leu Thr Ala Glu  
 2660 2665 2670  
 Asp Phe Arg Leu Leu Val Asn Gly Cys Gly Glu Val Asn Val Gln  
 2675 2680 2685  
 Met Leu Ile Ser Phe Thr Ser Phe Asn Asp Glu Ser Gly Glu Asn  
 2690 2695 2700  
 Ala Glu Lys Leu Leu Gln Phe Lys Arg Trp Phe Trp Ser Ile Val  
 2705 2710 2715  
 Glu Lys Met Ser Met Thr Glu Arg Gln Asp Leu Val Tyr Phe Trp  
 2720 2725 2730  
 Thr Ser Ser Pro Ser Leu Pro Ala Ser Glu Glu Gly Phe Gln Pro  
 2735 2740 2745  
 Met Pro Ser Ile Thr Ile Arg Pro Pro Asp Asp Gln His Leu Pro  
 2750 2755 2760  
 Thr Ala Asn Thr Cys Ile Ser Arg Leu Tyr Val Pro Leu Tyr Ser  
 2765 2770 2775  
 Ser Lys Gln Ile Leu Lys Gln Lys Leu Leu Leu Ala Ile Lys Thr  
 2780 2785 2790  
 Lys Asn Phe Gly Phe Val  
 2795

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<220>  
 <221> CDS  
 <222> (126)..(3359)

<400> 65  
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 gcctttccag catgcagggg ctgctcagcg tttagtcaca tcaagaaata gaacagaatt 120  
 cagcc atg gcc cca aga aag aga ggt gga cga ggt att tca ttc atc ttt 170  
 Met Ala Pro Arg Lys Arg Gly Gly Arg Gly Ile Ser Phe Ile Phe  
 1 5 10  
 tgc tgt ttc cga aat aat gat cac cca gaa atc acg tat cgg ctg cga 218  
 Cys Cys Phe Arg Asn Asn Asp His Pro Glu Ile Thr Tyr Arg Leu Arg  
 20 25 30  
 aat gat agc aac ttt gcg ctt cag acc atg gaa cca gca ttg ccc atg 266  
 Asn Asp Ser Asn Phe Ala Leu Gln Thr Met Glu Pro Ala Leu Pro Met  
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35

40

45

ccc	cct	gtg	gag	gag	ctg	gat	gtc	atg	ttc	agt	gaa	ctg	gtg	gat	gaa	314
Pro	Pro	Val	Glu	Glu	Leu	Asp	Val	Met	Phe	Ser	Glu	Leu	Val	Asp	Glu	
		50					55					60				
ctg	gac	ctc	aca	gac	aaa	cac	aga	gaa	gcc	atg	ttt	gca	ctt	cca	gct	362
Leu	Asp	Leu	Thr	Asp	Lys	His	Arg	Glu	Ala	Met	Phe	Ala	Leu	Pro	Ala	
	65					70					75					
gag	aaa	aaa	tgg	caa	ata	tac	tgt	agc	aag	aaa	aag	gac	cag	gaa	gaa	410
Glu	Lys	Lys	Trp	Gln	Ile	Tyr	Cys	Ser	Lys	Lys	Lys	Asp	Gln	Glu	Glu	
80					85				90					95		
aac	aag	gga	gct	aca	agt	tgg	cct	gaa	ttc	tac	att	gat	cag	ctc	aat	458
Asn	Lys	Gly	Ala	Thr	Ser	Trp	Pro	Glu	Phe	Tyr	Ile	Asp	Gln	Leu	Asn	
				100					105					110		
tcc	atg	gct	gct	aga	aaa	tct	ctg	ctg	gct	tta	gag	aag	gaa	gaa	gaa	506
Ser	Met	Ala	Ala	Arg	Lys	Ser	Leu	Leu	Ala	Leu	Glu	Lys	Glu	Glu	Glu	
			115					120					125			
gaa	gaa	aga	agt	aaa	act	ata	gag	agt	tta	aag	aca	gca	ctg	agg	aca	554
Glu	Glu	Arg	Ser	Lys	Thr	Ile	Glu	Ser	Leu	Lys	Thr	Ala	Leu	Arg	Thr	
		130					135					140				
aaa	cca	atg	agg	ttt	gta	acc	aga	ttc	atc	gac	ttg	gat	ggc	cta	tca	602
Lys	Pro	Met	Arg	Phe	Val	Thr	Arg	Phe	Ile	Asp	Leu	Asp	Gly	Leu	Ser	
	145					150					155					
tgt	atc	ctc	aac	ttt	cta	aag	acc	atg	gac	tac	gag	acc	tca	gag	tct	650
Cys	Ile	Leu	Asn	Phe	Leu	Lys	Thr	Met	Asp	Tyr	Glu	Thr	Ser	Glu	Ser	
160					165					170				175		
cga	ata	cat	act	tct	ctc	att	ggc	tgt	ata	aag	gcg	tta	atg	aac	aac	698
Arg	Ile	His	Thr	Ser	Leu	Ile	Gly	Cys	Ile	Lys	Ala	Leu	Met	Asn	Asn	
				180					185					190		
tct	caa	ggc	cgg	gct	cac	gtc	ctg	gct	cat	tct	gag	agt	att	aat	gta	746
Ser	Gln	Gly	Arg	Ala	His	Val	Leu	Ala	His	Ser	Glu	Ser	Ile	Asn	Val	
			195					200					205			
att	gct	cag	agt	ctg	agc	aca	gag	aac	att	aaa	acg	aag	gtg	gcc	gtg	794
Ile	Ala	Gln	Ser	Leu	Ser	Thr	Glu	Asn	Ile	Lys	Thr	Lys	Val	Ala	Val	
		210					215					220				
ctg	gaa	atc	ttg	ggc	gcc	gtg	tgc	ctg	gtt	ccc	ggg	ggc	cac	aag	aag	842
Leu	Glu	Ile	Leu	Gly	Ala	Val	Cys	Leu	Val	Pro	Gly	Gly	His	Lys	Lys	
	225					230					235					
gtt	ctg	cag	gcc	atg	ctg	cac	tac	cag	aag	tat	gcc	agc	gaa	agg	acc	890
Val	Leu	Gln	Ala	Met	Leu	His	Tyr	Gln	Lys	Tyr	Ala	Ser	Glu	Arg	Thr	
240					245					250					255	
cgc	ttt	cag	aca	tta	att	aac	gac	ttg	gat	aaa	agc	act	ggg	cgg	tat	938
Arg	Phe	Gln	Thr	Leu	Ile	Asn	Asp	Leu	Asp	Lys	Ser	Thr	Gly	Arg	Tyr	
				260					265					270		
cga	gat	gaa	gtg	agt	ctc	aag	act	gcc	atc	atg	tcc	ttc	att	aat	gca	986
Arg	Asp	Glu	Val	Ser	Leu	Lys	Thr	Ala	Ile	Met	Ser	Phe	Ile	Asn	Ala	
			275					280					285			
gtg	ctc	agc	caa	ggt	gca	gga	gtg	gag	agt	ttg	gac	ttt	aga	ctt	cat	1034
Val	Leu	Ser	Gln	Gly	Ala	Gly	Val	Glu	Ser	Leu	Asp	Phe	Arg	Leu	His	
		290					295					300				
ctt	cgc	tat	gaa	ttt	ctg	atg	tta	gga	att	caa	cct	gta	ata	gat	aaa	1082
Leu	Arg	Tyr	Glu	Phe	Leu	Met	Leu	Gly	Ile	Gln	Pro	Val	Ile	Asp	Lys	

## 122257 sequence listing May 10 2006.ST25.txt

305	310	315	
tta agg gaa cac gaa aat tca aca tta gat agg cat tta gac ttt ttt			1130
Leu Arg Glu His Glu Asn Ser Thr Leu Asp Arg His Leu Asp Phe Phe			
320	325	330	335
gaa atg ctc cga aat gaa gat gaa cta gaa ttt gcc aaa aga ttt gaa			1178
Glu Met Leu Arg Asn Glu Asp Glu Leu Glu Phe Ala Lys Arg Phe Glu			
	340	345	350
ctg gtt cac ata gac aca aaa agt gca act cag atg ttt gag ctg acc			1226
Leu Val His Ile Asp Thr Lys Ser Ala Thr Gln Met Phe Glu Leu Thr			
	355	360	365
agg aag agg ctg aca cat agt gaa gct tac ccg cat ttc atg tcc atc			1274
Arg Lys Arg Leu Thr His Ser Glu Ala Tyr Pro His Phe Met Ser Ile			
	370	375	380
ctg cac cac tgc ctc caa atg cct tac aag agg agt ggc aac act gtt			1322
Leu His His Cys Leu Gln Met Pro Tyr Lys Arg Ser Gly Asn Thr Val			
	385	390	395
cag tac tgg cta cta cta gat aga att ata cag cag ata gtt atc cag			1370
Gln Tyr Trp Leu Leu Leu Asp Arg Ile Ile Gln Gln Ile Val Ile Gln			
	400	405	410
aat gac aaa gga cag gac cct gac tcc aca cct ttg gaa aac ttt aat			1418
Asn Asp Lys Gly Gln Asp Pro Asp Ser Thr Thr Pro Leu Glu Asn Phe Asn			
	420	425	430
att aag aat gtc gta cga atg ttg gtt aat gaa aat gaa gtt aag cag			1466
Ile Lys Asn Val Val Arg Met Leu Val Asn Glu Asn Glu Val Lys Gln			
	435	440	445
tgg aaa gaa caa gcg gaa aaa atg aga aaa gag cac aat gag cta caa			1514
Trp Lys Glu Gln Ala Glu Lys Met Arg Lys Glu His Asn Glu Leu Gln			
	450	455	460
cag aaa ctg gaa aag aaa gaa cga gaa tgt gat gct aag act caa gag			1562
Gln Lys Leu Glu Lys Lys Glu Arg Glu Cys Asp Ala Lys Thr Gln Glu			
	465	470	475
aag gaa gag atg atg cag acc tta aat aaa atg aaa gag aaa ctt gaa			1610
Lys Glu Glu Met Met Gln Thr Leu Asn Lys Met Lys Glu Lys Leu Glu			
	480	485	490
aag gag act act gag cat aag caa gtc aag cag cag gtg gcg gac ctc			1658
Lys Glu Thr Thr Glu His Lys Gln Val Lys Gln Gln Val Ala Asp Leu			
	500	505	510
aca gca cag ctc cat gag ctc agc agg agg gcc gtc tgt gct tca atc			1706
Thr Ala Gln Leu His Glu Leu Ser Arg Arg Ala Val Cys Ala Ser Ile			
	515	520	525
cca ggt gga ccc tcg cct gga gca cca gga ggg ccc ttt cct tcc tct			1754
Pro Gly Gly Pro Ser Pro Gly Ala Pro Gly Gly Pro Phe Pro Ser Ser			
	530	535	540
gtg cct gga tct ctc ctt cct ccc cca cca ccc cca cct cta cca ggt			1802
Val Pro Gly Ser Leu Leu Pro Pro Pro Pro Pro Pro Pro Leu Pro Gly			
	545	550	555
ggg atg ctt ccc cct cca ccg cct ccc ctc cct cca ggt ggc cct cct			1850
Gly Met Leu Pro Pro Pro Pro Pro Pro Leu Pro Gly Gly Pro Pro			
	560	565	570
cct ccc cca ggg cct cct ccc tta ggg gca atc atg cca cct cct ggt			1898
Pro Pro Pro Gly Pro Pro Pro Leu Gly Ala Ile Met Pro Pro Pro Gly			



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580 585 590

gct cca atg ggc cta gca ctg aag aag aaa agc att cct cag ccc aca	1946
Ala Pro Met Gly Leu Ala Leu Lys Lys Lys Ser Ile Pro Gln Pro Thr	
595 600 605	
aat gcc ctg aaa tcc ttc aac tgg tct aaa ctg ccc gag aac aaa ctg	1994
Asn Ala Leu Lys Ser Phe Asn Trp Ser Lys Leu Pro Glu Asn Lys Leu	
610 615 620	
gaa gga aca gta tgg acc gaa att gat gat aca aaa gtc ttc aaa att	2042
Glu Gly Thr Val Trp Thr Glu Ile Asp Asp Thr Lys Val Phe Lys Ile	
625 630 635	
cta gat ctt gaa gac ctg gaa aga acc ttc tct gcc tat caa aga cag	2090
Leu Asp Leu Glu Asp Leu Glu Arg Thr Phe Ser Ala Tyr Gln Arg Gln	
640 645 650 655	
cag gat ttc ttt gtg aac agt aac tcc aag cag aaa gaa gca gat gcc	2138
Gln Asp Phe Phe Val Asn Ser Asn Ser Lys Gln Lys Glu Ala Asp Ala	
660 665 670	
att gat gac act ctg agt tcc aaa ctt aaa gtt aaa gag ctt tcg gtg	2186
Ile Asp Asp Thr Leu Ser Ser Lys Leu Lys Val Lys Glu Leu Ser Val	
675 680 685	
att gat ggt cgg aga gct cag aat tgc aac atc ctt cta tcg agg ttg	2234
Ile Asp Gly Arg Arg Ala Gln Asn Cys Asn Ile Leu Leu Ser Arg Leu	
690 695 700 705	
aaa tta tcc aat gac gaa atc aaa cgg gca att cta aca atg gac gaa	2282
Lys Leu Ser Asn Asp Glu Ile Lys Arg Ala Ile Leu Thr Met Asp Glu	
705 710 715	
cag gaa gat ctg ccc aag gac atg ttg gaa cag ctc ttg aaa ttt gtt	2330
Gln Glu Asp Leu Pro Lys Asp Met Leu Glu Gln Leu Leu Lys Phe Val	
720 725 730 735	
cct gaa aaa agt gac att gac cta ttg gag gaa cat aaa cac gaa ctg	2378
Pro Glu Lys Ser Asp Ile Asp Leu Leu Glu Glu His Lys His Glu Leu	
740 745 750	
gat cgg atg gcc aag gct gat agg ttc ctt ttt gag atg agc cga att	2426
Asp Arg Met Ala Lys Ala Asp Arg Phe Leu Phe Glu Met Ser Arg Ile	
755 760 765	
aat cac tat cag caa agg ttg caa tcg ctg tac ttc aaa aag aag ttt	2474
Asn His Tyr Gln Gln Arg Leu Gln Ser Leu Tyr Phe Lys Lys Lys Phe	
770 775 780	
gca gag cgt gtg gca gaa gtg aaa cct aaa gtg gaa gca att cgt tct	2522
Ala Glu Arg Val Ala Glu Val Lys Pro Lys Val Glu Ala Ile Arg Ser	
785 790 795	
ggc tca gaa gag gtg ttt agg agt ggt gcc ctc aag cag ttg ctg gag	2570
Gly Ser Glu Glu Val Phe Arg Ser Gly Ala Leu Lys Gln Leu Leu Glu	
800 805 810 815	
gtg gtt ttg gca ttt gga aat tat atg aat aaa ggt caa aga ggg aat	2618
Val Val Leu Ala Phe Gly Asn Tyr Met Asn Lys Gly Gln Arg Gly Asn	
820 825 830	
gca tat gga ttc aag ata tct agc cta aac aaa att gct gac aca aaa	2666
Ala Tyr Gly Phe Lys Ile Ser Ser Leu Asn Lys Ile Ala Asp Thr Lys	
835 840 845	
tcc agc atc gac aaa aac att acc ctt ttg cac tat ctc atc act att	2714
Ser Ser Ile Asp Lys Asn Ile Thr Leu Leu His Tyr Leu Ile Thr Ile	

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850	855	860	
gtg gaa aat aag tac ccc agt gtt ctc aat cta aat gaa gaa ttg cga Val Glu Asn Lys Tyr Pro Ser Val Leu Asn Leu Asn Glu Glu Leu Arg	865	870	875
gat att cct caa gct gcg aaa gta aac atg act gag ctg gac aaa gaa Asp Ile Pro Gln Ala Ala Lys Val Asn Met Thr Glu Leu Asp Lys Glu	880	885	890
ata agt acc ttg aga agt ggc ttg aaa gca gta gag aca gag ctg gaa Ile Ser Thr Leu Arg Ser Gly Leu Lys Ala Val Glu Thr Glu Leu Glu	900	905	910
tat cag aag tct cag ccc cca cag ccc gga gat aag ttt gtg tct gtt Tyr Gln Lys Ser Gln Pro Pro Gln Pro Gly Asp Lys Phe Val Ser Val	915	920	925
gtc agc cag ttc atc aca gta gcc agc ttc agc ttc tct gat gtt gaa Val Ser Gln Phe Ile Thr Val Ala Ser Phe Ser Phe Ser Asp Val Glu	930	935	940
gac ctt cta gca gaa gct aaa gac ctg ttt act aaa gca gtg aag cac Asp Leu Leu Ala Glu Ala Lys Asp Leu Phe Thr Lys Ala Val Lys His	945	950	955
ttt ggg gaa gag gct ggc aaa ata caa cca gat gag ttc ttt ggc att Phe Gly Glu Glu Ala Gly Lys Ile Gln Pro Asp Glu Phe Phe Gly Ile	960	965	970
ttt gat caa ttt ctt caa gct gtg tca gaa gcc aaa caa gaa aac gaa Phe Asp Gln Phe Leu Gln Ala Val Ser Glu Ala Lys Gln Glu Asn Glu	980	985	990
aat atg aga aag aaa aag gag gaa gaa gaa gaa cgt cga gct cgc atg gaa Asn Met Arg Lys Lys Lys Glu Glu Glu Glu Glu Arg Arg Ala Arg Met Glu	995	1000	1005
gct cag ctc aaa gaa caa cgt gaa agg gaa cgt aaa atg aga aaa Ala Gln Leu Lys Glu Gln Arg Glu Arg Glu Arg Lys Met Arg Lys	1010	1015	1020
gct aaa gag aat agt gaa gaa agc gga gag ttt gat gac ctt gtt Ala Lys Glu Asn Ser Glu Glu Ser Gly Glu Phe Asp Asp Leu Val	1025	1030	1035
tca gct tta cgc tca gga gaa gtg ttt gac aaa gac ctt tct aaa Ser Ala Leu Arg Ser Gly Glu Val Phe Asp Lys Asp Leu Ser Lys	1040	1045	1050
ttg aaa cgg aat cgc aaa cgt att acc aac cag atg act gac agc Leu Lys Arg Asn Arg Lys Arg Ile Thr Asn Gln Met Thr Asp Ser	1055	1060	1065
agc aga gag aga cca atc aca aaa ctt aat ttc taattttcca Ser Arg Glu Arg Pro Ile Thr Lys Leu Asn Phe	1070	1075	
tgaatacttt tttttagaaa gctcattagc agccctctaa agtgactaga acgtttcatt			3429
acactgcctt gcaatccaaa cagtggcaat tttttccttc atctgtgagt gaatgtgtga			3489
acgtgtgtat gtaaattgtat gtgtgtatat attaaaaaat gtatatagat gtctgagtgt			3549
tgtctggaga cctatacgta tggttaaaaa gatttatgtt aatgtatgtg ctccaaaacc			3609
tttcgtgtat gcattcacat tgagtgtggc tcattttctt tccccgaacg ccatgactgt			3669

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tcagaagcac aatactatct cctgaaagag ataagagaca ttccctagat tcaaaggcaa 3729  
aacagaagaa acaaacaaac aaacaaacaa agcttgcaaa atatatttatg gtttccaagc 3789  
ttgatatcct ttaaaattat tttcattgat ggaactggag ttgttgga aaacatagatt 3849  
taaaatgatt tttgatagct gacattgtga tggtgatgta tcacatcagt aataggacca 3909  
gctttgaatt tctgacattg gtgtggggat acagtctgta aatgtttatt gagaacatct 3969  
tgcacacaat ttgaattatg tagaatgtca atcaagtttt tgtatattta aaagttggac 4029  
atcaattttt tcccctgatt tcatcaagtt atctctgcc aagtgtcttg ataatttctt 4089  
cagatttttg gaaaaaaca ctatataaat gcaatccatg ctttttttaa agaacaacat 4149  
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tcaccaaga cttaaaggaa gaattctctg aagggataaa gattact 4256

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Cys Phe Arg Asn Asn Asp His Pro Glu Ile Thr Tyr Arg Leu Arg Asn  
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Asp Ser Asn Phe Ala Leu Gln Thr Met Glu Pro Ala Leu Pro Met Pro  
35 40 45

Pro Val Glu Glu Leu Asp Val Met Phe Ser Glu Leu Val Asp Glu Leu  
50 55 60

Asp Leu Thr Asp Lys His Arg Glu Ala Met Phe Ala Leu Pro Ala Glu  
65 70 75 80

Lys Lys Trp Gln Ile Tyr Cys Ser Lys Lys Lys Asp Gln Glu Glu Asn  
85 90 95

Lys Gly Ala Thr Ser Trp Pro Glu Phe Tyr Ile Asp Gln Leu Asn Ser  
100 105 110

Met Ala Ala Arg Lys Ser Leu Leu Ala Leu Glu Lys Glu Glu Glu Glu  
115 120 125

Glu Arg Ser Lys Thr Ile Glu Ser Leu Lys Thr Ala Leu Arg Thr Lys  
130 135 140

Pro Met Arg Phe Val Thr Arg Phe Ile Asp Leu Asp Gly Leu Ser Cys  
145 150 155 160

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Ile Leu Asn Phe Leu Lys Thr Met Asp Tyr Glu Thr Ser Glu Ser Arg  
165 170 175

Ile His Thr Ser Leu Ile Gly Cys Ile Lys Ala Leu Met Asn Asn Ser  
180 185 190

Gln Gly Arg Ala His Val Leu Ala His Ser Glu Ser Ile Asn Val Ile  
195 200 205

Ala Gln Ser Leu Ser Thr Glu Asn Ile Lys Thr Lys Val Ala Val Leu  
210 215 220

Glu Ile Leu Gly Ala Val Cys Leu Val Pro Gly Gly His Lys Lys Val  
225 230 235 240

Leu Gln Ala Met Leu His Tyr Gln Lys Tyr Ala Ser Glu Arg Thr Arg  
245 250 255

Phe Gln Thr Leu Ile Asn Asp Leu Asp Lys Ser Thr Gly Arg Tyr Arg  
260 265 270

Asp Glu Val Ser Leu Lys Thr Ala Ile Met Ser Phe Ile Asn Ala Val  
275 280 285

Leu Ser Gln Gly Ala Gly Val Glu Ser Leu Asp Phe Arg Leu His Leu  
290 295 300

Arg Tyr Glu Phe Leu Met Leu Gly Ile Gln Pro Val Ile Asp Lys Leu  
305 310 315 320

Arg Glu His Glu Asn Ser Thr Leu Asp Arg His Leu Asp Phe Phe Glu  
325 330 335

Met Leu Arg Asn Glu Asp Glu Leu Glu Phe Ala Lys Arg Phe Glu Leu  
340 345 350

Val His Ile Asp Thr Lys Ser Ala Thr Gln Met Phe Glu Leu Thr Arg  
355 360 365

Lys Arg Leu Thr His Ser Glu Ala Tyr Pro His Phe Met Ser Ile Leu  
370 375 380

His His Cys Leu Gln Met Pro Tyr Lys Arg Ser Gly Asn Thr Val Gln  
385 390 395 400

Tyr Trp Leu Leu Leu Asp Arg Ile Ile Gln Gln Ile Val Ile Gln Asn  
405 410 415

Asp Lys Gly Gln Asp Pro Asp Ser Thr Pro Leu Glu Asn Phe Asn Ile  
420 425 430

122257 sequence listing May 10 2006.ST25.txt

Lys Asn Val Val Arg Met Leu Val Asn Glu Asn Glu Val Lys Gln Trp  
435 440 445

Lys Glu Gln Ala Glu Lys Met Arg Lys Glu His Asn Glu Leu Gln Gln  
450 455 460

Lys Leu Glu Lys Lys Glu Arg Glu Cys Asp Ala Lys Thr Gln Glu Lys  
465 470 475 480

Glu Glu Met Met Gln Thr Leu Asn Lys Met Lys Glu Lys Leu Glu Lys  
485 490 495

Glu Thr Thr Glu His Lys Gln Val Lys Gln Gln Val Ala Asp Leu Thr  
500 505 510

Ala Gln Leu His Glu Leu Ser Arg Arg Ala Val Cys Ala Ser Ile Pro  
515 520 525

Gly Gly Pro Ser Pro Gly Ala Pro Gly Gly Pro Phe Pro Ser Ser Val  
530 535 540

Pro Gly Ser Leu Leu Pro Pro Pro Pro Pro Pro Pro Leu Pro Gly Gly  
545 550 555 560

Met Leu Pro Pro Pro Pro Pro Pro Leu Pro Pro Gly Gly Pro Pro Pro  
565 570 575

Pro Pro Gly Pro Pro Pro Leu Gly Ala Ile Met Pro Pro Pro Gly Ala  
580 585 590

Pro Met Gly Leu Ala Leu Lys Lys Lys Ser Ile Pro Gln Pro Thr Asn  
595 600 605

Ala Leu Lys Ser Phe Asn Trp Ser Lys Leu Pro Glu Asn Lys Leu Glu  
610 615 620

Gly Thr Val Trp Thr Glu Ile Asp Asp Thr Lys Val Phe Lys Ile Leu  
625 630 635 640

Asp Leu Glu Asp Leu Glu Arg Thr Phe Ser Ala Tyr Gln Arg Gln Gln  
645 650 655

Asp Phe Phe Val Asn Ser Asn Ser Lys Gln Lys Glu Ala Asp Ala Ile  
660 665 670

Asp Asp Thr Leu Ser Ser Lys Leu Lys Val Lys Glu Leu Ser Val Ile  
675 680 685

Asp Gly Arg Arg Ala Gln Asn Cys Asn Ile Leu Leu Ser Arg Leu Lys  
690 695 700

122257 sequence listing May 10 2006.ST25.txt

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Leu Ser Asn Asp Glu Ile Lys Arg Ala Ile Leu Thr Met Asp Glu Gln
705          710          715          720

Glu Asp Leu Pro Lys Asp Met Leu Glu Gln Leu Leu Lys Phe Val Pro
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Glu Lys Ser Asp Ile Asp Leu Leu Glu Glu His Lys His Glu Leu Asp
          740          745          750

Arg Met Ala Lys Ala Asp Arg Phe Leu Phe Glu Met Ser Arg Ile Asn
          755          760          765

His Tyr Gln Gln Arg Leu Gln Ser Leu Tyr Phe Lys Lys Lys Phe Ala
          770          775          780

Glu Arg Val Ala Glu Val Lys Pro Lys Val Glu Ala Ile Arg Ser Gly
785          790          795          800

Ser Glu Glu Val Phe Arg Ser Gly Ala Leu Lys Gln Leu Leu Glu Val
          805          810          815

Val Leu Ala Phe Gly Asn Tyr Met Asn Lys Gly Gln Arg Gly Asn Ala
          820          825          830

Tyr Gly Phe Lys Ile Ser Ser Leu Asn Lys Ile Ala Asp Thr Lys Ser
          835          840          845

Ser Ile Asp Lys Asn Ile Thr Leu Leu His Tyr Leu Ile Thr Ile Val
          850          855          860

Glu Asn Lys Tyr Pro Ser Val Leu Asn Leu Asn Glu Glu Leu Arg Asp
865          870          875          880

Ile Pro Gln Ala Ala Lys Val Asn Met Thr Glu Leu Asp Lys Glu Ile
          885          890          895

Ser Thr Leu Arg Ser Gly Leu Lys Ala Val Glu Thr Glu Leu Glu Tyr
          900          905          910

Gln Lys Ser Gln Pro Pro Gln Pro Gly Asp Lys Phe Val Ser Val Val
          915          920          925

Ser Gln Phe Ile Thr Val Ala Ser Phe Ser Phe Ser Asp Val Glu Asp
          930          935          940

Leu Leu Ala Glu Ala Lys Asp Leu Phe Thr Lys Ala Val Lys His Phe
945          950          955          960

Gly Glu Glu Ala Gly Lys Ile Gln Pro Asp Glu Phe Phe Gly Ile Phe
          965          970          975

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122257 sequence listing May 10 2006.ST25.txt

Asp Gln Phe Leu Gln Ala Val Ser Glu Ala Lys Gln Glu Asn Glu Asn  
980 985 990

Met Arg Lys Lys Lys Glu Glu Glu Glu Arg Arg Ala Arg Met Glu Ala  
995 1000 1005

Gln Leu Lys Glu Gln Arg Glu Arg Glu Arg Lys Met Arg Lys Ala  
1010 1015 1020

Lys Glu Asn Ser Glu Glu Ser Gly Glu Phe Asp Asp Leu Val Ser  
1025 1030 1035

Ala Leu Arg Ser Gly Glu Val Phe Asp Lys Asp Leu Ser Lys Leu  
1040 1045 1050

Lys Arg Asn Arg Lys Arg Ile Thr Asn Gln Met Thr Asp Ser Ser  
1055 1060 1065

Arg Glu Arg Pro Ile Thr Lys Leu Asn Phe  
1070 1075

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gtg atg agc ccc tgt gga ggt gaa gac att gtg gct gac cac gtt gcc	96
Val Met Ser Pro Cys Gly Gly Glu Asp Ile Val Ala Asp His Val Ala	
20 25 30	
tct tgt ggt gta aac ttg tac cag ttt tac ggt ccc tct ggc cag tac	144
Ser Cys Gly Val Asn Leu Tyr Gln Phe Tyr Gly Pro Ser Gly Gln Tyr	
35 40 45	
acc cat gaa ttt gat gga gat gag cag ttc tac gtg gac ctg gag agg	192
Thr His Glu Phe Asp Gly Asp Glu Gln Phe Tyr Val Asp Leu Glu Arg	
50 55 60	
aag gag act gcc tgg cgg tgg cct gag ttc agc aaa ttt gga ggt ttt	240
Lys Glu Thr Ala Trp Arg Trp Pro Glu Phe Ser Lys Phe Gly Gly Phe	
65 70 75 80	
gac ccg cag ggt gca ctg aga aac atg gct gtg gca aaa cac aac ttg	288
Asp Pro Gln Gly Ala Leu Arg Asn Met Ala Val Ala Lys His Asn Leu	
85 90 95	
aac atc atg att aaa cgc tac aac tct acc gct gct acc aat gag gtt	336
Asn Ile Met Ile Lys Arg Tyr Asn Ser Thr Ala Ala Thr Asn Glu Val	
100 105 110	
cct gag gtc aca gtg ttt tcc aag tct ccc gtg aca ctg ggt cag ccc	384

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Pro	Glu	Val	Thr	Val	Phe	Ser	Lys	Ser	Pro	Val	Thr	Leu	Gly	Gln	Pro		
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Asn	Thr	Leu	Ile	Cys	Leu	Val	Asp	Asn	Ile	Phe	Pro	Pro	Val	Val	Asn		
		130				135					140						
atc	aca	tgg	ctg	agc	aat	ggg	cag	tca	gtc	aca	gaa	ggg	gtt	tct	gag	480	
Ile	Thr	Trp	Leu	Ser	Asn	Gly	Gln	Ser	Val	Thr	Glu	Gly	Val	Ser	Glu		
		145			150					155					160		
acc	agc	ttc	ctc	tcc	aag	agt	gat	cat	tcc	ttc	ttc	aag	atc	agt	tac	528	
Thr	Ser	Phe	Leu	Ser	Lys	Ser	Asp	His	Ser	Phe	Phe	Lys	Ile	Ser	Tyr		
				165					170					175			
ctc	acc	ttc	ctc	cct	tct	gct	gat	gag	att	tat	gac	tgc	aag	gtg	gag	576	
Leu	Thr	Phe	Leu	Pro	Ser	Ala	Asp	Glu	Ile	Tyr	Asp	Cys	Lys	Val	Glu		
			180					185					190				
cac	tgg	ggc	ctg	gac	cag	cct	ctt	ctg	aaa	cac	tgg	gag	cct	gag	att	624	
His	Trp	Gly	Leu	Asp	Gln	Pro	Leu	Leu	Lys	His	Trp	Glu	Pro	Glu	Ile		
		195					200					205					
cca	gcc	cct	atg	tca	gag	ctc	aca	gag	act	gtg	gtc	tgt	gcc	ctg	ggg	672	
Pro	Ala	Pro	Met	Ser	Glu	Leu	Thr	Glu	Thr	Val	Val	Cys	Ala	Leu	Gly		
		210				215					220						
ttg	tct	gtg	ggc	ctc	atg	ggc	att	gtg	gtg	ggc	act	gtc	ttc	atc	atc	720	
Leu	Ser	Val	Gly	Leu	Met	Gly	Ile	Val	Val	Gly	Thr	Val	Phe	Ile	Ile		
		225			230					235					240		
caa	ggc	ctg	cgt	tca	gtt	ggg	gct	tcc	aga	cac	caa	ggg	cca	ttg		765	
Gln	Gly	Leu	Arg	Ser	Val	Gly	Ala	Ser	Arg	His	Gln	Gly	Pro	Leu			
				245					250					255			
tgaatcccat	cctggaagg	aagggtgcatc	gccatctaca	ggagcagaag	aatggacttg											825	
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tttctcctct	caccttttct	ctgggactta	agctgctata	tcccctcaga	gctcacaat											945	
gcctttacat	tctttccctg	acctcctgat	tttttttttc	ttttctcaaa	tgttacctac											1005	
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 <212> PRT  
 <213> homo sapiens

<400> 68

Met Ile Leu Asn Lys Ala Leu Leu Leu Gly Ala Leu Ala Leu Thr Thr  
 1 5 10 15

Val Met Ser Pro Cys Gly Gly Glu Asp Ile Val Ala Asp His Val Ala  
 20 25 30

Ser Cys Gly Val Asn Leu Tyr Gln Phe Tyr Gly Pro Ser Gly Gln Tyr  
 35 40 45

Thr His Glu Phe Asp Gly Asp Glu Gln Phe Tyr Val Asp Leu Glu Arg  
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50

55

60

Lys Glu Thr Ala Trp Arg Trp Pro Glu Phe Ser Lys Phe Gly Gly Phe  
 65 70 75 80

Asp Pro Gln Gly Ala Leu Arg Asn Met Ala Val Ala Lys His Asn Leu  
 85 90 95

Asn Ile Met Ile Lys Arg Tyr Asn Ser Thr Ala Ala Thr Asn Glu Val  
 100 105 110

Pro Glu Val Thr Val Phe Ser Lys Ser Pro Val Thr Leu Gly Gln Pro  
 115 120 125

Asn Thr Leu Ile Cys Leu Val Asp Asn Ile Phe Pro Pro Val Val Asn  
 130 135 140

Ile Thr Trp Leu Ser Asn Gly Gln Ser Val Thr Glu Gly Val Ser Glu  
 145 150 155 160

Thr Ser Phe Leu Ser Lys Ser Asp His Ser Phe Phe Lys Ile Ser Tyr  
 165 170 175

Leu Thr Phe Leu Pro Ser Ala Asp Glu Ile Tyr Asp Cys Lys Val Glu  
 180 185 190

His Trp Gly Leu Asp Gln Pro Leu Leu Lys His Trp Glu Pro Glu Ile  
 195 200 205

Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Val Val Cys Ala Leu Gly  
 210 215 220

Leu Ser Val Gly Leu Met Gly Ile Val Val Gly Thr Val Phe Ile Ile  
 225 230 235 240

Gln Gly Leu Arg Ser Val Gly Ala Ser Arg His Gln Gly Pro Leu  
 245 250 255

<210> 69  
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 <212> DNA  
 <213> homo sapiens

<220>  
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<400> 69  
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 aaactctcct gcgccccaga agatttcttc ctcggcgaag ggacagcgaa agatgagggt 180

## 122257 sequence listing May 10 2006.ST25.txt

ggcaggaaga gaaggcgctt tctgtctgcc ggggtcgcag cgcgagaggg cagtgcc	237
atg ttc ctc tcc atc cta gtg gcg ctg tgc ctg tgg ctg cac ctg gcg Met Phe Leu Ser Ile Leu Val Ala Leu Cys Leu Trp Leu His Leu Ala 1 5 10 15	285
ctg ggc gtg cgc ggc gcg ccc tgc gag gcg gtg cgc atc cct atg tgc Leu Gly Val Arg Gly Ala Pro Cys Glu Ala Val Arg Ile Pro Met Cys 20 25 30	333
cgg cac atg ccc tgg aac atc acg cgg atg ccc aac cac ctg cac cac Arg His Met Pro Trp Asn Ile Thr Arg Met Pro Asn His Leu His His 35 40 45	381
agc acg cag gag aac gcc atc ctg gcc atc gag cag tac gag gag ctg Ser Thr Gln Glu Asn Ala Ile Leu Ala Ile Glu Gln Tyr Glu Glu Leu 50 55 60	429
gtg gac gtg aac tgc agc gcc gtg ctg cgc ttc ttc ttc tgt gcc atg Val Asp Val Asn Cys Ser Ala Val Leu Arg Phe Phe Phe Cys Ala Met 65 70 75 80	477
tac gcg ccc att tgc acc ctg gag ttc ctg cac gac cct atc aag ccg Tyr Ala Pro Ile Cys Thr Leu Glu Phe Leu His Asp Pro Ile Lys Pro 85 90 95	525
tgc aag tcg gtg tgc caa cgc gcg cgc gac gac tgc gag ccc ctc atg Cys Lys Ser Val Cys Gln Arg Ala Arg Asp Asp Cys Glu Pro Leu Met 100 105 110	573
aag atg tac aac cac agc tgg ccc gaa agc ctg gcc tgc gac gag ctg Lys Met Tyr Asn His Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu 115 120 125	621
cct gtc tat gac cgt ggc gtg tgc att tcg cct gaa gcc atc gtc acg Pro Val Tyr Asp Arg Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr 130 135 140	669
gac ctc ccg gag gat gtt aag tgg ata gac atc aca cca gac atg atg Asp Leu Pro Glu Asp Val Lys Trp Ile Asp Ile Thr Pro Asp Met Met 145 150 155 160	717
gta cag gaa agg cct ctt gat gtt gac tgt aaa cgc cta agc ccc gat Val Gln Glu Arg Pro Leu Asp Val Asp Cys Lys Arg Leu Ser Pro Asp 165 170 175	765
cgg tgc aag tgt aaa aag gtg aag cca act ttg gca acg tat ctc agc Arg Cys Lys Cys Lys Lys Val Lys Pro Thr Leu Ala Thr Tyr Leu Ser 180 185 190	813
aaa aac tac agc tat gtt att cat gcc aaa ata aaa gct gtg cag agg Lys Asn Tyr Ser Tyr Val Ile His Ala Lys Ile Lys Ala Val Gln Arg 195 200 205	861
agt ggc tgc aat gag gtc aca acg gtg gtg gat gta aaa gag atc ttc Ser Gly Cys Asn Glu Val Thr Thr Val Val Asp Val Lys Glu Ile Phe 210 215 220	909
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tct tct tgc cag tgt cca cac atc ctg ccc cat caa gat gtt ctc atc Ser Ser Cys Gln Cys Pro His Ile Leu Pro His Gln Asp Val Leu Ile 245 250 255	1005
atg tgt tac gag tgg cgt tca agg atg atg ctt ctt gaa aat tgc tta Met Cys Tyr Glu Trp Arg Ser Arg Met Met Leu Leu Glu Asn Cys Leu 260 265 270 275 280 285 290 295 300	1053

ggt gaa aaa tgg aga gat cag ctt agt aaa aga tcc ata cag tgg gaa	1101
Val Glu Lys Trp Arg Asp Gln Leu Ser Lys Arg Ser Ile Gln Trp Glu	
275 280 285	
gag agg ctg cag gaa cag cgg aga aca gtt cag gac aag aag aaa aca	1149
Glu Arg Leu Gln Glu Gln Arg Arg Thr Val Gln Asp Lys Lys Lys Thr	
290 295 300	
gcc ggg cgc acc agt cgt agt aat ccc ccc aaa cca aag gga aag cct	1197
Ala Gly Arg Thr Ser Arg Ser Asn Pro Pro Lys Pro Lys Gly Lys Pro	
305 310 315 320	
cct gct ccc aaa cca gcc agt ccc aag aag aac att aaa act agg agt	1245
Pro Ala Pro Lys Pro Ala Ser Pro Lys Lys Asn Ile Lys Thr Arg Ser	
325 330 335	
gcc cag aag aga aca aac ccg aaa aga gtg tgagctaact agtttccaaa	1295
Ala Gln Lys Arg Thr Asn Pro Lys Arg Val	
340 345	
gcggagactt ccgacttcct tacaggatga ggctgggcat tgcctgggac agcctatgta	1355
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gcatttttct taaggctatg cttcagtttt tctttgtaag ccatcacaag ccatagtggg	1475
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cgacctaata tgtgcattgt aaaataaatg ccatatttca aacaaaacac gtaatttttt	1655
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tatgtgttta tggctctgag aaggattttt gtgatgaaag gggatttttt gaaaaattag	1835
agaagtagca tatggaaaaat tataatgtgt ttttttacca atgacttcag tttctgtttt	1895
tagctagaaa cttaaaaaaca aaaataataa taaagaaaaa taaataaaaa ggagaggcag	1955
acaatgtctg gattcctgtt ttttggttac ctgattttcca tgatcatgat gcttcttgtc	2015
aacaccctct taagcagcac cagaaacagt gagtttgtct gtaccattag gagttaggta	2075
ctaattagtt ggctaattgct caagtatttt ataccacaa gagaggtatg tcactcatct	2135
tacttcccag gacatccacc ctgagaataa tttgacaagc ttaaaaatgg cttcatgtg	2195
agtgccaaat tttgtttttc ttcatttaaa tattttcttt gcctaaatac atgtgagagg	2255
agttaaatat aaatgtacag agaggaaagt tgagttccac ctctgaaatg agaattactt	2315
gacagttggg atactttaat cagaaaaaaa gaacttatgt gcagcatttt atcaacaaat	2375
ttcataattg tggacaattg gaggcattta ttttaaaaaa caattttatt ggccttttgc	2435
taacacagta agcatgtatt ttataaggca ttcaataaat gcacaacgcc caaaggaaat	2495
aaaatcctat ctaatcctac tctccactac acagaggtaa tcactattag tattttggca	2555
tattattctc caggtgtttg cttatgcact tataaaatga tttgaacaaa taaaactagg	2615
aacctgtata catgtgtttc ataacctgcc tcctttgctt ggccctttat tgagataagt	2675

122257 sequence listing May 10 2006.ST25.txt

tttcctgtca agaaagcaga aaccatctca tttctaacag ctgtgttata ttccatagta 2735  
 tgcattactc aacaaactgt tgtgctattg gatacttagg tggtttcttc actgacaata 2795  
 ctgaataaac atctcaccgg aattc 2820

<210> 70  
 <211> 346  
 <212> PRT  
 <213> homo sapiens

<400> 70

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Leu Gly Val Arg Gly Ala Pro Cys Glu Ala Val Arg Ile Pro Met Cys  
 20 25 30

Arg His Met Pro Trp Asn Ile Thr Arg Met Pro Asn His Leu His His  
 35 40 45

Ser Thr Gln Glu Asn Ala Ile Leu Ala Ile Glu Gln Tyr Glu Glu Leu  
 50 55 60

Val Asp Val Asn Cys Ser Ala Val Leu Arg Phe Phe Phe Cys Ala Met  
 65 70 75 80

Tyr Ala Pro Ile Cys Thr Leu Glu Phe Leu His Asp Pro Ile Lys Pro  
 85 90 95

Cys Lys Ser Val Cys Gln Arg Ala Arg Asp Asp Cys Glu Pro Leu Met  
 100 105 110

Lys Met Tyr Asn His Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu  
 115 120 125

Pro Val Tyr Asp Arg Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr  
 130 135 140

Asp Leu Pro Glu Asp Val Lys Trp Ile Asp Ile Thr Pro Asp Met Met  
 145 150 155 160

Val Gln Glu Arg Pro Leu Asp Val Asp Cys Lys Arg Leu Ser Pro Asp  
 165 170 175

Arg Cys Lys Cys Lys Lys Val Lys Pro Thr Leu Ala Thr Tyr Leu Ser  
 180 185 190

Lys Asn Tyr Ser Tyr Val Ile His Ala Lys Ile Lys Ala Val Gln Arg  
 195 200 205

Ser Gly Cys Asn Glu Val Thr Thr Val Val Asp Val Lys Glu Ile Phe  
 210 215 220

122257 sequence listing May 10 2006.ST25.txt

Lys Ser Ser Ser Pro Ile Pro Arg Thr Gln Val Pro Leu Ile Thr Asn  
 225 230 235 240  
 Ser Ser Cys Gln Cys Pro His Ile Leu Pro His Gln Asp Val Leu Ile  
 245 250 255  
 Met Cys Tyr Glu Trp Arg Ser Arg Met Met Leu Leu Glu Asn Cys Leu  
 260 265 270  
 Val Glu Lys Trp Arg Asp Gln Leu Ser Lys Arg Ser Ile Gln Trp Glu  
 275 280 285  
 Glu Arg Leu Gln Glu Gln Arg Arg Thr Val Gln Asp Lys Lys Lys Thr  
 290 295 300  
 Ala Gly Arg Thr Ser Arg Ser Asn Pro Pro Lys Pro Lys Gly Lys Pro  
 305 310 315 320  
 Pro Ala Pro Lys Pro Ala Ser Pro Lys Lys Asn Ile Lys Thr Arg Ser  
 325 330 335  
 Ala Gln Lys Arg Thr Asn Pro Lys Arg Val  
 340 345

<210> 71  
 <211> 1362  
 <212> DNA  
 <213> homo sapiens

<220>  
 <221> CDS  
 <222> (50)..(1066)

<400> 71  
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 Met Ser Thr  
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 Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Asp His Ser Thr  
 5 10 15  
 ccc cca agt gca tat ggg tct gtc aaa gcc tat act aac ttt gat gct 154  
 Pro Pro Ser Ala Tyr Gly Ser Val Lys Ala Tyr Thr Asn Phe Asp Ala  
 20 25 30 35  
 gag cgg gat gct ttg aac att gaa aca gcc atc aag acc aaa ggt gtg 202  
 Glu Arg Asp Ala Leu Asn Ile Glu Thr Ala Ile Lys Thr Lys Gly Val  
 40 45 50  
 gat gag gtc acc att gtc aac att ttg acc aac cgc agc aat gca cag 250  
 Asp Glu Val Thr Ile Val Asn Ile Leu Thr Asn Arg Ser Asn Ala Gln  
 55 60 65  
 aga cag gat att gcc ttc gcc tac cag aga agg acc aaa aag gaa ctt 298  
 Arg Gln Asp Ile Ala Phe Ala Tyr Gln Arg Arg Thr Lys Lys Glu Leu  
 70 75 80

## 122257 sequence listing May 10 2006.ST25.txt

gca tca gca ctg aag tca gcc tta tct ggc cac ctg gag acg gtg att Ala Ser Ala Leu Lys Ser Ala Leu Ser Gly His Leu Glu Thr Val Ile 85 90 95	346
tgt ggc cta ttg aag aca cct gct cag tat gac gct tct gag cta aaa Leu Gly Leu Leu Lys Thr Pro Ala Gln Tyr Asp Ala Ser Glu Leu Lys 100 105 110 115	394
gct tcc atg aag ggg ctg gga acc gac gag gac tct ctc att gag atc Ala Ser Met Lys Gly Leu Gly Thr Asp Glu Asp Ser Leu Ile Glu Ile 120 125 130	442
atc tgc tcc aga acc aac cag gag ctg cag gaa att aac aga gtc tac Ile Cys Ser Arg Thr Asn Gln Glu Leu Gln Glu Ile Asn Arg Val Tyr 135 140 145	490
aag gaa atg tac aag act gat ctg gag aag gac att att tcg gac aca Lys Glu Met Tyr Lys Thr Asp Leu Glu Lys Asp Ile Ile Ser Asp Thr 150 155 160	538
tct ggt gac ttc cgc aag ctg atg gtt gcc ctg gca aag ggt aga aga Ser Gly Asp Phe Arg Lys Leu Met Val Ala Leu Ala Lys Gly Arg Arg 165 170 175	586
gca gag gat ggc tct gtc att gat tat gaa ctg att gac caa gat gct Ala Glu Asp Gly Ser Val Ile Asp Tyr Glu Leu Ile Asp Gln Asp Ala 180 185 190 195	634
cgg gat ctc tat gac gct gga gtg aag agg aaa gga act gat gtt ccc Arg Asp Leu Tyr Asp Ala Gly Val Lys Arg Lys Gly Thr Asp Val Pro 200 205 210	682
aag tgg atc agc atc atg acc gag cgg agc gtg ccc cac ctc cag aaa Lys Trp Ile Ser Ile Met Thr Glu Arg Ser Val Pro His Leu Gln Lys 215 220 225	730
gta ttt gat agg tac aag agt tac agc cct tat gac atg ttg gaa agc Val Phe Asp Arg Tyr Lys Ser Tyr Ser Pro Tyr Asp Met Leu Glu Ser 230 235 240	778
atc agg aaa gag gtt aaa gga gac ctg gaa aat gct ttc ctg aac ctg Ile Arg Lys Glu Val Lys Gly Asp Leu Glu Asn Ala Phe Leu Asn Leu 245 250 255	826
gtt cag tgc att cag aac aag ccc ctg tat ttt gct gat cgg ctg tat Val Gln Cys Ile Gln Asn Lys Pro Leu Tyr Phe Ala Asp Arg Leu Tyr 260 265 270 275	874
gac tcc atg aag ggc aag ggg acg cga gat aag gtc ctg atc aga atc Asp Ser Met Lys Gly Lys Gly Thr Arg Asp Lys Val Leu Ile Arg Ile 280 285 290	922
atg gtc tcc cgc agt gaa gtg gac atg ttg aaa att agg tct gaa ttc Met Val Ser Arg Ser Glu Val Asp Met Leu Lys Ile Arg Ser Glu Phe 295 300 305	970
aag aga aag tac ggc aag tcc ctg tac tat tat atc cag caa gac act Lys Arg Lys Tyr Gly Lys Ser Leu Tyr Tyr Tyr Ile Gln Gln Asp Thr 310 315 320	1018
aag ggc gac tac cag aaa gcg ctg ctg tac ctg tgt ggt gga gat gac Lys Gly Asp Tyr Gln Lys Ala Leu Leu Tyr Leu Cys Gly Gly Asp Asp 325 330 335	1066
tgaagcccga cacggcctga gcgtccagaa atggtgctca ccatgcttcc agctaacagg	1126
tctagaaaac cagcttgcca ataacagtcc ccgtggccat ccctgtgagg gtgacgttag	1186

122257 sequence listing May 10 2006.ST25.txt

cattaccccc aacctcattt tagttgccta agcattgcct ggccttcctg tctagtctct 1246  
cctgtaagcc aaagaaatga acattccaag gagttggaag tgaagtctat gatgtgaaac 1306  
actttgcctc ctgtgtactg tgtcataaac agatgaataa actgaatttg tactttt 1362

<210> 72  
<211> 339  
<212> PRT  
<213> homo sapiens

<400> 72

Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Asp  
1 5 10 15

His Ser Thr Pro Pro Ser Ala Tyr Gly Ser Val Lys Ala Tyr Thr Asn  
20 25 30

Phe Asp Ala Glu Arg Asp Ala Leu Asn Ile Glu Thr Ala Ile Lys Thr  
35 40 45

Lys Gly Val Asp Glu Val Thr Ile Val Asn Ile Leu Thr Asn Arg Ser  
50 55 60

Asn Ala Gln Arg Gln Asp Ile Ala Phe Ala Tyr Gln Arg Arg Thr Lys  
65 70 75 80

Lys Glu Leu Ala Ser Ala Leu Lys Ser Ala Leu Ser Gly His Leu Glu  
85 90 95

Thr Val Ile Leu Gly Leu Leu Lys Thr Pro Ala Gln Tyr Asp Ala Ser  
100 105 110

Glu Leu Lys Ala Ser Met Lys Gly Leu Gly Thr Asp Glu Asp Ser Leu  
115 120 125

Ile Glu Ile Ile Cys Ser Arg Thr Asn Gln Glu Leu Gln Glu Ile Asn  
130 135 140

Arg Val Tyr Lys Glu Met Tyr Lys Thr Asp Leu Glu Lys Asp Ile Ile  
145 150 155 160

Ser Asp Thr Ser Gly Asp Phe Arg Lys Leu Met Val Ala Leu Ala Lys  
165 170 175

Gly Arg Arg Ala Glu Asp Gly Ser Val Ile Asp Tyr Glu Leu Ile Asp  
180 185 190

Gln Asp Ala Arg Asp Leu Tyr Asp Ala Gly Val Lys Arg Lys Gly Thr  
195 200 205

Asp Val Pro Lys Trp Ile Ser Ile Met Thr Glu Arg Ser Val Pro His  
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210

215

220

Leu Gln Lys Val Phe Asp Arg Tyr Lys Ser Tyr Ser Pro Tyr Asp Met  
 225 230 235 240

Leu Glu Ser Ile Arg Lys Glu Val Lys Gly Asp Leu Glu Asn Ala Phe  
 245 250 255

Leu Asn Leu Val Gln Cys Ile Gln Asn Lys Pro Leu Tyr Phe Ala Asp  
 260 265 270

Arg Leu Tyr Asp Ser Met Lys Gly Lys Gly Thr Arg Asp Lys Val Leu  
 275 280 285

Ile Arg Ile Met Val Ser Arg Ser Glu Val Asp Met Leu Lys Ile Arg  
 290 295 300

Ser Glu Phe Lys Arg Lys Tyr Gly Lys Ser Leu Tyr Tyr Tyr Ile Gln  
 305 310 315 320

Gln Asp Thr Lys Gly Asp Tyr Gln Lys Ala Leu Leu Tyr Leu Cys Gly  
 325 330 335

Gly Asp Asp

<210> 73  
 <211> 850  
 <212> DNA  
 <213> homo sapiens

<220>  
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 <222> (107)..(781)

<400> 73  
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gcagctgcag ccgcccgcgc gcagatccac gctggctccg tgcgcc atg gtc acc 115  
 Met Val Thr  
 1

cac agc aag ttt ccc gcc gcc ggg atg agc cgc ccc ctg gac acc agc 163  
 His Ser Lys Phe Pro Ala Ala Gly Met Ser Arg Pro Leu Asp Thr Ser  
 5 10 15

ctg cgc ctc aag acc ttc agc tcc aag agc gag tac cag ctg gtg gtg 211  
 Leu Arg Leu Lys Thr Phe Ser Ser Lys Ser Glu Tyr Gln Leu Val Val  
 20 25 30 35

aac gca gtg cgc aag ctg cag gag agc ggc ttc tac tgg agc gca gtg 259  
 Asn Ala Val Arg Lys Leu Gln Glu Ser Gly Phe Tyr Trp Ser Ala Val  
 40 45 50

acc ggc ggc gag gcg aac ctg ctg ctc agt gcc gag ccc gcc ggc acc 307  
 Thr Gly Gly Glu Ala Asn Leu Leu Leu Ser Ala Glu Pro Ala Gly Thr  
 55 60 65



122257 sequence listing May 10 2006.ST25.txt

ttt	ctg	atc	cgc	gac	agc	tcg	gac	cag	cgc	cac	ttc	ttc	acg	ctc	agc	355
Phe	Leu	Ile	Arg	Asp	Ser	Ser	Asp	Gln	Arg	His	Phe	Phe	Thr	Leu	Ser	
		70					75					80				
gtc	aag	acc	cag	tct	ggg	acc	aag	aac	ctg	cgc	atc	cag	tgt	gag	ggg	403
Val	Lys	Thr	Gln	Ser	Gly	Thr	Lys	Asn	Leu	Arg	Ile	Gln	Cys	Glu	Gly	
	85					90					95					
ggc	agc	ttc	tct	ctg	cag	agc	gat	ccc	cgg	agc	acg	cag	ccc	gtg	ccc	451
Gly	Ser	Phe	Ser	Leu	Gln	Ser	Asp	Pro	Arg	Ser	Thr	Gln	Pro	Val	Pro	
100					105					110					115	
cgc	ttc	gac	tgc	gtg	ctc	aag	ctg	gtg	tac	cac	tac	atg	ccg	ccc	cct	499
Arg	Phe	Asp	Cys	Val	Leu	Lys	Leu	Val	Tyr	His	Tyr	Met	Pro	Pro	Pro	
				120					125					130		
gga	gcc	ccc	tcc	ttc	ccc	tcg	cca	cct	act	gaa	ccc	tcc	tcc	gag	gtg	547
Gly	Ala	Pro	Ser	Phe	Pro	Ser	Pro	Pro	Thr	Glu	Pro	Ser	Ser	Glu	Val	
			135					140					145			
ccc	gag	cag	ccg	tct	gcc	cag	cca	ctc	cct	ggg	agt	ccc	ccc	aga	aga	595
Pro	Glu	Gln	Pro	Ser	Ala	Gln	Pro	Leu	Pro	Gly	Ser	Pro	Pro	Arg	Arg	
		150					155					160				
gcc	tat	tac	atc	tac	tcc	ggg	ggc	gag	aag	atc	ccc	ctg	gtg	ttg	agc	643
Ala	Tyr	Tyr	Ile	Tyr	Ser	Gly	Gly	Glu	Lys	Ile	Pro	Leu	Val	Leu	Ser	
	165					170					175					
cgg	ccc	ctc	tcc	tcc	aac	gtg	gcc	act	ctt	cag	cat	ctc	tgt	cgg	aag	691
Arg	Pro	Leu	Ser	Ser	Asn	Val	Ala	Thr	Leu	Gln	His	Leu	Cys	Arg	Lys	
180					185					190					195	
acc	gtc	aac	ggc	cac	ctg	gac	tcc	tat	gag	aaa	gtc	acc	cag	ctg	ccg	739
Thr	Val	Asn	Gly	His	Leu	Asp	Ser	Tyr	Glu	Lys	Val	Thr	Gln	Leu	Pro	
				200					205					210		
ggg	ccc	att	cgg	gag	ttc	ctg	gac	cag	tac	gat	gcc	ccg	ctt			781
Gly	Pro	Ile	Arg	Glu	Phe	Leu	Asp	Gln	Tyr	Asp	Ala	Pro	Leu			
			215					220					225			
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gtggcacat																850

<210> 74  
 <211> 225  
 <212> PRT  
 <213> homo sapiens

<400> 74

Met Val Thr His Ser Lys Phe Pro Ala Ala Gly Met Ser Arg Pro Leu  
 1 5 10 15

Asp Thr Ser Leu Arg Leu Lys Thr Phe Ser Ser Lys Ser Glu Tyr Gln  
 20 25 30

Leu Val Val Asn Ala Val Arg Lys Leu Gln Glu Ser Gly Phe Tyr Trp  
 35 40 45

Ser Ala Val Thr Gly Gly Glu Ala Asn Leu Leu Leu Ser Ala Glu Pro  
 50 55 60

122257 sequence listing May 10 2006.ST25.txt

Ala Gly Thr Phe Leu Ile Arg Asp Ser Ser Asp Gln Arg His Phe Phe  
65 70 75 80

Thr Leu Ser Val Lys Thr Gln Ser Gly Thr Lys Asn Leu Arg Ile Gln  
85 90 95

Cys Glu Gly Gly Ser Phe Ser Leu Gln Ser Asp Pro Arg Ser Thr Gln  
100 105 110

Pro Val Pro Arg Phe Asp Cys Val Leu Lys Leu Val Tyr His Tyr Met  
115 120 125

Pro Pro Pro Gly Ala Pro Ser Phe Pro Ser Pro Pro Thr Glu Pro Ser  
130 135 140

Ser Glu Val Pro Glu Gln Pro Ser Ala Gln Pro Leu Pro Gly Ser Pro  
145 150 155 160

Pro Arg Arg Ala Tyr Tyr Ile Tyr Ser Gly Gly Glu Lys Ile Pro Leu  
165 170 175

Val Leu Ser Arg Pro Leu Ser Ser Asn Val Ala Thr Leu Gln His Leu  
180 185 190

Cys Arg Lys Thr Val Asn Gly His Leu Asp Ser Tyr Glu Lys Val Thr  
195 200 205

Gln Leu Pro Gly Pro Ile Arg Glu Phe Leu Asp Gln Tyr Asp Ala Pro  
210 215 220

Leu  
225

<210> 75  
<211> 369  
<212> DNA  
<213> homo sapiens

<220>  
<221> CDS  
<222> (1)..(366)

<400> 75	
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Met Lys Leu Leu Thr Gly Leu Val Phe Cys Ser Leu Val Leu Gly Val	
1 5 10 15	
agc agc cga agc ttc ttt tcg ttc ctt ggc gag gct ttt gat ggg gct	96
Ser Ser Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala	
20 25 30	
cgg gac atg tgg aga gcc tac tct gac atg aga gaa gcc aat tac atc	144
Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile	
35 40 45	
ggc tca gac aaa tac ttc cat gct cgg ggg aac tat gat gct gcc aaa	192

122257 sequence listing May 10 2006.ST25.txt

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Gly Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys
 50                               55                               60

agg gga cct ggg ggt gtc tgg gct gca gaa gcg atc agc gat gcc aga      240
Arg Gly Pro Ala Gly Val Trp Ala Ala Glu Ala Ile Ser Asp Ala Arg
65                               70                               75

gag aat atc cag aga ttc ttt ggc cat ggt gcg gag gac tcg ctg gct      288
Glu Asn Ile Gln Arg Phe Phe Gly His Gly Ala Glu Asp Ser Leu Ala
85                               90                               95

gat cag gct gcc aat gaa tgg ggc agg agt ggc aaa gac ccc aat cac      336
Asp Gln Ala Ala Asn Glu Trp Gly Arg Ser Gly Lys Asp Pro Asn His
100                             105                             110

ttc cga cct gct ggc ctg cct gag aaa tac tga      369
Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr
115                             120

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<210> 76  
 <211> 122  
 <212> PRT  
 <213> homo sapiens

<400> 76

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Met Lys Leu Leu Thr Gly Leu Val Phe Cys Ser Leu Val Leu Gly Val
 1                               5                               10                               15

Ser Ser Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala
20                               25                               30

Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile
35                               40                               45

Gly Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys
50                               55                               60

Arg Gly Pro Gly Gly Val Trp Ala Ala Glu Ala Ile Ser Asp Ala Arg
65                               70                               75

Glu Asn Ile Gln Arg Phe Phe Gly His Gly Ala Glu Asp Ser Leu Ala
85                               90                               95

Asp Gln Ala Ala Asn Glu Trp Gly Arg Ser Gly Lys Asp Pro Asn His
100                             105                             110

Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr
115                             120

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<210> 77  
 <211> 895  
 <212> DNA  
 <213> homo sapiens

<220>  
 <221> CDS  
 <222> (147)..(497)

122257 sequence listing May 10 2006.ST25.txt

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<400> 77
gcgggccgcgt cgaccggcgc ggctggagcg cagcgccgaa gggactggca gggctgaagt      60
gtgcggggaca gcaagcccc gaatagcccc ggctgccacc tcgcaggacc caaggccacg      120
cgcgccgggc ccagctgagc cgcctc atg aag ccg ccc gcg gag gac ctg tcg      173
                               Met Lys Pro Pro Ala Glu Asp Leu Ser
                               1                               5

gac gcg ctg tgc gag ttt gac gcg gtg ctg gcc gac ttc gcg tcg ccc      221
Asp Ala Leu Cys Glu Phe Asp Ala Val Leu Ala Asp Phe Ala Ser Pro
10                               15                               20                               25

ttc cac gag cgc cac ttc cac tac gag gag cac ctg gag cgc atg aag      269
Phe His Glu Arg His Phe His Tyr Glu Glu His Leu Glu Arg Met Lys
                               30                               35                               40

cgg cgc agc agc gcc agt gtc agc gac agc agc ggc ttc agc gac tcg      317
Arg Arg Ser Ser Ala Ser Val Ser Asp Ser Ser Gly Phe Ser Asp Ser
                               45                               50                               55

gag agt gca gat tca ctt tat agg aac agc ttc agc ttc agt gat gaa      365
Glu Ser Ala Asp Ser Leu Tyr Arg Asn Ser Phe Ser Phe Ser Asp Glu
60                               65                               70

aaa ctg aat tct cca aca gac tct acc cca gct ctt ctc tct gcc act      413
Lys Leu Asn Ser Pro Thr Asp Ser Thr Pro Ala Leu Leu Ser Ala Thr
75                               80                               85

gtc act cct cag aaa gct aaa tta gga gac aca aaa gag cta gaa gcc      461
Val Thr Pro Gln Lys Ala Lys Leu Gly Asp Thr Lys Glu Leu Glu Ala
90                               95                               100                               105

ttc att gct gat ctt gac aaa act tta gca agt atg tgaaacaaga      507
Phe Ile Ala Asp Leu Asp Lys Thr Leu Ala Ser Met
                               110                               115

agtttctgggt cttttcatca taaggagaaa gcttcagaaa gttccgagga cctgctaaaa      567
tcagctacta gaatctgctg ccagagggga caaagacgtg cactcaacct tctaccaggc      627
cactctcagg ctcaccttaa aatcagccct tgatccatt tctgggcaat ttagacagtg      687
aaactgactt tgtttacctg cttgcagcat attagaacag acgatccatg ctaatattgt      747
attttctctt aaaacatagc tttcctgtaa tttaaagtgc ttttatgaaa atatttgtaa      807
ttaattatat atagttggaa atagcagtaa gctttcccat tataatatat ttttgatac      867
aaataaaatt tgaactgaac ctgctgcc      895

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<210> 78
<211> 117
<212> PRT
<213> homo sapiens

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<400> 78
Met Lys Pro Pro Ala Glu Asp Leu Ser Asp Ala Leu Cys Glu Phe Asp
1                               5                               10                               15

Ala Val Leu Ala Asp Phe Ala Ser Pro Phe His Glu Arg His Phe His
20                               25                               30

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122257 sequence listing May 10 2006.ST25.txt

Tyr Glu Glu His Leu Glu Arg Met Lys Arg Arg Ser Ser Ala Ser Val  
35 40 45

Ser Asp Ser Ser Gly Phe Ser Asp Ser Glu Ser Ala Asp Ser Leu Tyr  
50 55 60

Arg Asn Ser Phe Ser Phe Ser Asp Glu Lys Leu Asn Ser Pro Thr Asp  
65 70 75 80

Ser Thr Pro Ala Leu Leu Ser Ala Thr Val Thr Pro Gln Lys Ala Lys  
85 90 95

Leu Gly Asp Thr Lys Glu Leu Glu Ala Phe Ile Ala Asp Leu Asp Lys  
100 105 110

Thr Leu Ala Ser Met  
115

<210> 79  
<211> 1564  
<212> DNA  
<213> homo sapiens

<220>  
<221> CDS  
<222> (314)..(1138)

<400> 79  
gaagcacatc tggacagctg tgcggcctcc ttgcgggccc acgtcagccg agcacgtccc 60  
ccacgtcctc tccttctcgc cacttattat ttattcgttt tcccaaagaa gcgactaggg 120  
acccaagttt aaaaattcct cccccactc aatgcgagac gtggccagat cccatccaac 180  
acacggttta attttcatgg ggctctggga tcaaaagaac agaaacagca acaacaaaag 240  
cccagccgct gtctgatttt aagctggcaa agtgggaaaa ataaagtgtt gagtaaacag 300  
accaagttgg atc atg ggg aat ttc aga ggt cat gcc ctc cct gga acc 349  
Met Gly Asn Phe Arg Gly His Ala Leu Pro Gly Thr  
1 5 10  
ttc ttt ttt att att ggt ctt tgg tgg tgt aca aag agt att ctg aag 397  
Phe Phe Phe Ile Ile Gly Leu Trp Trp Cys Thr Lys Ser Ile Leu Lys  
15 20 25  
tat atc tgc aaa aag caa aag cga acc tgc tat ctt ggt tcc aaa aca 445  
Tyr Ile Cys Lys Lys Gln Lys Arg Thr Cys Tyr Leu Gly Ser Lys Thr  
30 35 40  
tta ttc tat cga ttg gaa att ttg gag gga att aca ata gtt ggc atg 493  
Leu Phe Tyr Arg Leu Glu Ile Leu Glu Gly Ile Thr Ile Val Gly Met  
45 50 55 60  
gct tta act ggc atg gct ggg gag cag ttt att cct gga ggg ccc cat 541  
Ala Leu Thr Gly Met Ala Gly Glu Gln Phe Ile Pro Gly Gly Pro His  
65 70 75  
ctg atg tta tat gac tat aaa caa ggt cac tgg aat caa ctc ctg ggc 589  
Leu Met Leu Tyr Asp Tyr Lys Gln Gly His Trp Asn Gln Leu Leu Gly  
80 85 90

122257 sequence listing May 10 2006.ST25.txt

tgg cat cat ttc acc atg tat ttc ttc ttt ggg ctg ttg ggt gtg gca Trp His His Phe Thr Met Tyr Phe Phe Phe Gly Leu Leu Gly Val Ala 95 100 105	637
gat atc tta tgt ttc acc atc agt tca ctt cct gtg tcc tta acc aag Asp Ile Leu Cys Phe Thr Ile Ser Ser Leu Pro Val Ser Leu Thr Lys 110 115 120	685
tta atg ttg tca aat gcc tta ttt gtg gag gcc ttt atc ttc tac aac Leu Met Leu Ser Asn Ala Leu Phe Val Glu Ala Phe Ile Phe Tyr Asn 125 130 135 140	733
cac act cat ggc cgg gaa atg ctg gac atc ttt gtg cac cag ctg ctg His Thr His Gly Arg Glu Met Leu Asp Ile Phe Val His Gln Leu Leu 145 150 155	781
gtt ttg gtc gtc ttt ctg aca ggc ctc gtt gcc ttc cta gag ttc ctt Val Leu Val Val Phe Leu Thr Gly Leu Val Ala Phe Leu Glu Phe Leu 160 165 170	829
gtt cgg aac aat gta ctt ctg gag cta ttg cgg tca agt ctc att ctg Val Arg Asn Asn Val Leu Leu Glu Leu Leu Arg Ser Ser Leu Ile Leu 175 180 185	877
ctt cag ggg agc tgg ttc ttt cag att gga ttt gtc ctg tat ccc ccc Leu Gln Gly Ser Trp Phe Phe Gln Ile Gly Phe Val Leu Tyr Pro Pro 190 195 200	925
agt gga ggt cct gca tgg gat ctg atg gat cat gaa aat att ttg ttt Ser Gly Gly Pro Ala Trp Asp Leu Met Asp His Glu Asn Ile Leu Phe 205 210 215 220	973
ctc acc ata tgc ttt tgt tgg cat tat gca gta acc att gtc atc gtt Leu Thr Ile Cys Phe Cys Trp His Tyr Ala Val Thr Ile Val Ile Val 225 230 235	1021
gga atg aat tat gct ttc att acc tgg ttg gtt aaa tct aga ctt aag Gly Met Asn Tyr Ala Phe Ile Thr Trp Leu Val Lys Ser Arg Leu Lys 240 245 250	1069
agg ctc tgc tcc tca gaa gtt gga ctt ctg aaa aat gct gaa cga gaa Arg Leu Cys Ser Ser Glu Val Gly Leu Leu Lys Asn Ala Glu Arg Glu 255 260 265	1117
caa gaa tca gaa gaa gaa atg tgactttgat gagcttccag tttttctaga Gln Glu Ser Glu Glu Glu Met 270 275	1168
taaacctttt cttttttaca ttgttcttgg ttttgtttct cgatcttttg tttggagaac	1228
agctggctaa ggatgactct aagtgtactg tttgcatttc caatttggtt aaagtatttg	1288
aatttaaata ttttcttttt agctttgaaa atattttggg tgatactttc attttgcaca	1348
tcatgcacat catggtattc aggggctaga gtgatttttt tccagattat ctaaagttgg	1408
atgccccacac tatgaaagaa atatttgttt tatttgcctt atagatatgc tcaaggttac	1468
tgggcttgct actatttgta actccttgac catggaatta tacttgttta tcttgttgct	1528
gcaatgagaa ataaatgaat gtatgtattt tgggtgc	1564

<210> 80  
 <211> 275  
 <212> PRT  
 <213> homo sapiens

122257 sequence listing May 10 2006.ST25.txt

<400> 80

Met Gly Asn Phe Arg Gly His Ala Leu Pro Gly Thr Phe Phe Phe Ile  
1 5 10 15

Ile Gly Leu Trp Trp Cys Thr Lys Ser Ile Leu Lys Tyr Ile Cys Lys  
20 25 30

Lys Gln Lys Arg Thr Cys Tyr Leu Gly Ser Lys Thr Leu Phe Tyr Arg  
35 40 45

Leu Glu Ile Leu Glu Gly Ile Thr Ile Val Gly Met Ala Leu Thr Gly  
50 55 60

Met Ala Gly Glu Gln Phe Ile Pro Gly Gly Pro His Leu Met Leu Tyr  
65 70 75 80

Asp Tyr Lys Gln Gly His Trp Asn Gln Leu Leu Gly Trp His His Phe  
85 90 95

Thr Met Tyr Phe Phe Phe Gly Leu Leu Gly Val Ala Asp Ile Leu Cys  
100 105 110

Phe Thr Ile Ser Ser Leu Pro Val Ser Leu Thr Lys Leu Met Leu Ser  
115 120 125

Asn Ala Leu Phe Val Glu Ala Phe Ile Phe Tyr Asn His Thr His Gly  
130 135 140

Arg Glu Met Leu Asp Ile Phe Val His Gln Leu Leu Val Leu Val Val  
145 150 155 160

Phe Leu Thr Gly Leu Val Ala Phe Leu Glu Phe Leu Val Arg Asn Asn  
165 170 175

Val Leu Leu Glu Leu Leu Arg Ser Ser Leu Ile Leu Leu Gln Gly Ser  
180 185 190

Trp Phe Phe Gln Ile Gly Phe Val Leu Tyr Pro Pro Ser Gly Gly Pro  
195 200 205

Ala Trp Asp Leu Met Asp His Glu Asn Ile Leu Phe Leu Thr Ile Cys  
210 215 220

Phe Cys Trp His Tyr Ala Val Thr Ile Val Ile Val Gly Met Asn Tyr  
225 230 235 240

Ala Phe Ile Thr Trp Leu Val Lys Ser Arg Leu Lys Arg Leu Cys Ser  
245 250 255

Ser Glu Val Gly Leu Leu Lys Asn Ala Glu Arg Glu Gln Glu Ser Glu  
Page 199

Glu Glu Met  
275

<210> 81  
<211> 2311  
<212> DNA  
<213> homo sapiens

<220>  
<221> CDS  
<222> (199)..(876)

<400> 81  
gatttaatcc tatgacaaac taagttggtt ctgtcttcac ctgttttggt gaggttgtgt 60  
aagagttggt gtttgctcag gaagagattt aagcatgctt gcttaccag actcagagaa 120  
gtctccctgt tctgtcctag ctatgttcct gtgttggtgtg cattcgtctt ttccagagca 180  
aaccgcccag agtagaag atg gat tgg ggc acg ctg cag acg atc ctg ggg 231  
Met Asp Trp Gly Thr Leu Gln Thr Ile Leu Gly  
1 5 10  
ggt gtg aac aaa cac tcc acc agc att gga aag atc tgg ctc acc gtc 279  
Gly Val Asn Lys His Ser Thr Ser Ile Gly Lys Ile Trp Leu Thr Val  
15 20 25  
ctc ttc att ttt cgc att atg atc ctc gtt gtg gct gca aag gag gtg 327  
Leu Phe Ile Phe Arg Ile Met Ile Leu Val Val Ala Ala Lys Glu Val  
30 35 40  
tgg gga gat gag cag gcc gac ttt gtc tgc aac acc ctg cag cca ggc 375  
Trp Gly Asp Glu Gln Ala Asp Phe Val Cys Asn Thr Leu Gln Pro Gly  
45 50 55  
tgc aag aac gtg tgc tac gat cac tac ttc ccc atc tcc cac atc cgg 423  
Cys Lys Asn Val Cys Tyr Asp His Tyr Phe Pro Ile Ser His Ile Arg  
60 65 70 75  
cta tgg gcc ctg cag ctg atc ttc gtg tcc agc cca gcg ctc cta gtg 471  
Leu Trp Ala Leu Gln Leu Ile Phe Val Ser Ser Pro Ala Leu Leu Val  
80 85 90  
gcc atg cac gtg gcc tac cgg aga cat gag aag aag agg aag ttc atc 519  
Ala Met His Val Ala Tyr Arg Arg His Glu Lys Lys Arg Lys Phe Ile  
95 100 105  
aag ggg gag ata aag agt gaa ttt aag gac atc gag gag atc aaa acc 567  
Lys Gly Glu Ile Lys Ser Glu Phe Lys Asp Ile Glu Glu Ile Lys Thr  
110 115 120  
cag aag gtc cgc atc gaa ggc tcc ctg tgg tgg acc tac aca agc agc 615  
Gln Lys Val Arg Ile Glu Gly Ser Leu Trp Trp Thr Tyr Thr Ser Ser  
125 130 135  
atc ttc ttc cgg gtc atc ttc gaa gcc gcc ttc atg tac gtc ttc tat 663  
Ile Phe Phe Arg Val Ile Phe Glu Ala Ala Phe Met Tyr Val Phe Tyr  
140 145 150 155  
gtc atg tac gac ggc ttc tcc atg cag cgg ctg gtg aag tgc aac gcc 711  
Val Met Tyr Asp Gly Phe Ser Met Gln Arg Leu Val Lys Cys Asn Ala  
160 165 170



122257 sequence listing May 10 2006.ST25.txt

tgg cct tgt ccc aac act gtg gac tgc ttt gtg tcc cgg ccc acg gag	759
Trp Pro Cys Pro Asn Thr Val Asp Cys Phe Val Ser Arg Pro Thr Glu	
175 180 185	
aag act gtc ttc aca gtg ttc atg att gca gtg tct gga att tgc atc	807
Lys Thr Val Phe Thr Val Phe Met Ile Ala Val Ser Gly Ile Cys Ile	
190 195 200	
ctg ctg aat gtc act gaa ttg tgt tat ttg cta att aga tat tgt tct	855
Leu Leu Asn Val Thr Glu Leu Cys Tyr Leu Leu Ile Arg Tyr Cys Ser	
205 210 215	
ggg aag tca aaa aag cca gtt taacgcattg cccagttggt agattaagaa	906
Gly Lys Ser Lys Lys Pro Val	
220 225	
atagacagca tgagagggat gaggcaaccc gtgctcagct gtcaaggctc agtcgccagc	966
atttcccaac acaaagattc tgaccttaaa tgcaaccatt tgaaaccctt gtaggcctca	1026
ggtgaaactc cagatgccac aatgagctct gctcccctaa agcctcaaaa caaaggccta	1086
attctatgcc tgtcttaatt ttctttcact taagttagtt ccaactgagac cccaggctgt	1146
taggggttat tgggtgtaagg tactttcata ttttaaacag aggatatcgg catttgtttc	1206
tttctctgag gacaagagaa aaaagccagg ttccacagag gacacagaga aggtttgggt	1266
gtcctcctgg ggttcttttt gccaaactttc cccacgttaa aggtgaacat tggttctttc	1326
atttgctttg gaagttttta tctctaacag tggacaaagt taccagtgcc ttaaactctg	1386
ttacactttt tggaagtga aactttgtag tatgataggt tattttgatg taaagatggt	1446
ctggatacca ttatatgttc cccctgtttc agaggctcag attgtaatat gtaaattggt	1506
tgtcattcgc tactatgatt taatttgaaa tatggctctt tggttatgaa tactttgcag	1566
cacagctgag agaggctgtc tgttgatttc attgtggtca tagcacctaa caacattgta	1626
gcctcaatcg agtgagacag actagaagtt cctagttggc ttatgatagc aaatggcctc	1686
atgtcaaata ttagatgtaa ttttgtgtaa gaaatacaga ctggatgtac caccaactac	1746
tacctgtaat gacaggcctg tccaacacat ctcccttttc catgctgtgg tagccagcat	1806
cggaaagaac gctgatttaa agaggtgagc ttgggaattt tattgacaca gtaccattta	1866
atggggagac aaaaatgggg gccaggggag ggagaagttt ctgtcgtaa aaacgagttt	1926
ggaaagactg gactctaaat tctgttgatt aaagatgagc tttgtctacc ttcaaaagtt	1986
tgtttggtt acccccttca gcctccaatt ttttaagtga aaatataact aataacatgt	2046
gaaaagaata gaagctaagg tttagataaa tattgagcag atctatagga agattgaacc	2106
tgaatatattgc cattatgctt gacatggttt ccaaaaaatg gtactccaca tacttcagtg	2166
agggtaagta ttttcctgtt gtcaagaata gcattgtaaa agcattttgt aataataaag	2226
aatagcttta atgatatgct tgtaactaaa ataattttgt aatgtatcaa atacatttaa	2286
aacattaaaa tataatctct ataatt	2311

<210> 82  
 <211> 226  
 <212> PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 82

Met Asp Trp Gly Thr Leu Gln Thr Ile Leu Gly Gly Val Asn Lys His  
 1 5 10 15

Ser Thr Ser Ile Gly Lys Ile Trp Leu Thr Val Leu Phe Ile Phe Arg  
 20 25 30

Ile Met Ile Leu Val Val Ala Ala Lys Glu Val Trp Gly Asp Glu Gln  
 35 40 45

Ala Asp Phe Val Cys Asn Thr Leu Gln Pro Gly Cys Lys Asn Val Cys  
 50 55 60

Tyr Asp His Tyr Phe Pro Ile Ser His Ile Arg Leu Trp Ala Leu Gln  
 65 70 75 80

Leu Ile Phe Val Ser Ser Pro Ala Leu Leu Val Ala Met His Val Ala  
 85 90 95

Tyr Arg Arg His Glu Lys Lys Arg Lys Phe Ile Lys Gly Glu Ile Lys  
 100 105 110

Ser Glu Phe Lys Asp Ile Glu Glu Ile Lys Thr Gln Lys Val Arg Ile  
 115 120 125

Glu Gly Ser Leu Trp Trp Thr Tyr Thr Ser Ser Ile Phe Phe Arg Val  
 130 135 140

Ile Phe Glu Ala Ala Phe Met Tyr Val Phe Tyr Val Met Tyr Asp Gly  
 145 150 155 160

Phe Ser Met Gln Arg Leu Val Lys Cys Asn Ala Trp Pro Cys Pro Asn  
 165 170 175

Thr Val Asp Cys Phe Val Ser Arg Pro Thr Glu Lys Thr Val Phe Thr  
 180 185 190

Val Phe Met Ile Ala Val Ser Gly Ile Cys Ile Leu Leu Asn Val Thr  
 195 200 205

Glu Leu Cys Tyr Leu Leu Ile Arg Tyr Cys Ser Gly Lys Ser Lys Lys  
 210 215 220

Pro Val  
 225

&lt;210&gt; 83

&lt;211&gt; 2389

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

122257 sequence listing May 10 2006.ST25.txt

<220>

<221> CDS

<222> (73)..(1143)

<400> 83

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Met Gln Ser Val Gln Ser Thr Ser Phe Cys Leu Arg Lys  
1 5 10

cag tgc ctt tgc ctg acc ttc ctg ctt ctc cat ctc ctg gga cag gtc 159  
Gln Cys Leu Cys Leu Thr Phe Leu Leu Leu His Leu Leu Gly Gln Val  
15 20 25

gct gcg act cag cgc tgc cct ccc cag tgc ccg ggc cgg tgc cct gcg 207  
Ala Ala Thr Gln Arg Cys Pro Pro Gln Cys Pro Gly Arg Cys Pro Ala  
30 35 40 45

acg ccg ccg acc tgc gcc ccc ggg gtg cgc gcg gtg ctg gac ggc tgc 255  
Thr Pro Pro Thr Cys Ala Pro Gly Val Arg Ala Val Leu Asp Gly Cys  
50 55 60

tca tgc tgt ctg gtg tgt gcc cgc cag cgt ggc gag agc tgc tca gat 303  
Ser Cys Cys Leu Val Cys Ala Arg Gln Arg Gly Glu Ser Cys Ser Asp  
65 70 75

ctg gag cca tgc gac gag agc agt ggc ctc tac tgt gat cgc agc gcg 351  
Leu Glu Pro Cys Asp Glu Ser Ser Gly Leu Tyr Cys Asp Arg Ser Ala  
80 85 90

gac ccc agc aac cag act ggc atc tgc acg gcg gta gag gga gat aac 399  
Asp Pro Ser Asn Gln Thr Gly Ile Cys Thr Ala Val Glu Gly Asp Asn  
95 100 105

tgt gtg ttc gat ggg gtc atc tac cgc agt gga gag aaa ttt cag cca 447  
Cys Val Phe Asp Gly Val Ile Tyr Arg Ser Gly Glu Lys Phe Gln Pro  
110 115 120 125

agc tgc aaa ttc cag tgc acc tgc aga gat ggg cag att ggc tgt gtg 495  
Ser Cys Lys Phe Gln Cys Thr Cys Arg Asp Gly Gln Ile Gly Cys Val  
130 135 140

ccc cgc tgt cag ctg gat gtg cta ctg cct gag cct aac tgc cca gct 543  
Pro Arg Cys Gln Leu Asp Val Leu Leu Pro Glu Pro Asn Cys Pro Ala  
145 150 155

cca aga aaa gtt gag gtg cct gga gag tgc tgt gaa aag tgg atc tgt 591  
Pro Arg Lys Val Glu Val Pro Gly Glu Cys Cys Glu Lys Trp Ile Cys  
160 165 170

ggc cca gat gag gag gat tca ctg gga ggc ctt acc ctt gca gct tac 639  
Gly Pro Asp Glu Glu Asp Ser Leu Gly Gly Leu Thr 185  
175 180

agg cca gaa gcc acc cta gga gta gaa gtc tct gac tca agt gtc aac 687  
Arg Pro Glu Ala Thr Leu Gly Val Glu Val Ser Asp Ser Ser Val Asn  
190 195 200 205

tgc att gaa cag acc aca gag tgg aca gca tgc tcc aag agc tgt ggt 735  
Cys Ile Glu Gln Thr Thr Glu Trp Thr Ala Cys Ser Lys Ser Cys Gly  
210 215 220

atg ggg ttc tcc acc cgg gtc acc aat agg aac cgt caa tgt gag atg 783  
Met Gly Phe Ser Thr Arg Val Thr Asn Arg Asn Arg Gln Cys Glu Met  
225 230 235

## 122257 sequence listing May 10 2006.ST25.txt

ctg aaa cag act cgg ctc tgc atg gtg cgg ccc tgt gaa caa gag cca Leu Lys Gln Thr Arg Leu Cys Met Val Arg Pro Cys Glu Gln Glu Pro 240 245 250	831
gag cag cca aca gat aag aaa gga aaa aag tgt ctc cgc acc aag aag Glu Gln Pro Thr Asp Lys Lys Gly Lys Lys Cys Leu Arg Thr Lys Lys 255 260 265	879
tca ctc aaa gcc atc cac ctg cag ttc aag aac tgc acc agc ctg cac Ser Leu Lys Ala Ile His Leu Gln Phe Lys Asn Cys Thr Ser Leu His 270 275 280 285	927
acc tac aag ccc agg ttc tgt ggg gtc tgc agt gat ggc cgc tgc tgc Thr Tyr Lys Pro Arg Phe Cys Gly Val Cys Ser Asp Gly Arg Cys Cys 290 295 300	975
act ccc cac aat acc aaa acc atc cag gca gag ttt cag tgc tcc cca Thr Pro His Asn Thr Lys Thr Ile Gln Ala Glu Phe Gln Cys Ser Pro 305 310 315	1023
ggg caa ata gtc aag aag cca gtg atg gtc att ggg acc tgc acc tgt Gly Gln Ile Val Lys Lys Pro Val Met Val Ile Gly Thr Cys Thr Cys 320 325 330	1071
cac acc aac tgt cct aag aac aat gag gcc ttc ctc cag gag ctg gag His Thr Asn Cys Pro Lys Asn Asn Glu Ala Phe Leu Gln Glu Leu Glu 335 340 345	1119
ctg aag act acc aga ggg aaa atg taacctatca ctcaagaagc acacctacag Leu Lys Thr Thr Arg Gly Lys Met 350 355	1173
agcacctgta gctgctgcgc caccacccat caaaggaata taagaaaagt aatgaagaat	1233
cacgatttca tccttgaatc ctatgtatctt tcctaattgtg atcatatgag gacctttcat	1293
atctgtcttt tatttaacaa aaaatgtaat taactgtaaa cttggaatca aggtaagctc	1353
aggatatggc ttaggaatga cttactttcc tgtggtttta ttacaaatgc aaatttctat	1413
aaatttaaga aaacaagtat ataatttact ttgtagactg tttcacattg cactcatcat	1473
attttgttgt gcactagtgc aattccaaga aaatatcact gtaatgagtc agtgaagtct	1533
agaatcatac ttaacatttc attgtacaag tattacaacc atatattgag gttcattggg	1593
aagattctct attggctccc tttttgggta aaccagctct gaacttccaa gtcctcaaatc	1653
caaggaaaca tgcagctctt caacatgaca tccagagatg actattactt ttctgtttag	1713
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Gln Arg Cys Pro Pro Gln Cys Pro Gly Arg Cys Pro Ala Thr Pro Pro  
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Thr Cys Ala Pro Gly Val Arg Ala Val Leu Asp Gly Cys Ser Cys Cys  
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Leu Val Cys Ala Arg Gln Arg Gly Glu Ser Cys Ser Asp Leu Glu Pro  
65 70 75 80

Cys Asp Glu Ser Ser Gly Leu Tyr Cys Asp Arg Ser Ala Asp Pro Ser  
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Asn Gln Thr Gly Ile Cys Thr Ala Val Glu Gly Asp Asn Cys Val Phe  
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Asp Gly Val Ile Tyr Arg Ser Gly Glu Lys Phe Gln Pro Ser Cys Lys  
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Phe Gln Cys Thr Cys Arg Asp Gly Gln Ile Gly Cys Val Pro Arg Cys  
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Gln Leu Asp Val Leu Leu Pro Glu Pro Asn Cys Pro Ala Pro Arg Lys  
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Val Glu Val Pro Gly Glu Cys Cys Glu Lys Trp Ile Cys Gly Pro Asp  
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Glu Glu Asp Ser Leu Gly Gly Leu Thr Leu Ala Ala Tyr Arg Pro Glu  
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195 200 205

Gln Thr Thr Glu Trp Thr Ala Cys Ser Lys Ser Cys Gly Met Gly Phe  
Page 205

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Ser Thr Arg Val Thr Asn Arg Asn Arg Gln Cys Glu Met Leu Lys Gln  
225 230 235 240

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Thr Asp Lys Lys Gly Lys Lys Cys Leu Arg Thr Lys Lys Ser Leu Lys  
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Pro Arg Phe Cys Gly Val Cys Ser Asp Gly Arg Cys Cys Thr Pro His  
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Val Lys Lys Pro Val Met Val Ile Gly Thr Cys Thr Cys His Thr Asn  
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Cys Pro Lys Asn Asn Glu Ala Phe Leu Gln Glu Leu Glu Leu Lys Thr  
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Thr Arg Gly Lys Met  
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